

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:26:33 ; Search time 85 Seconds
(without alignments)
7978.235 Million cell updates/sec

Title: US-10-019-661-1
Perfect score: 1222
Sequence: 1 cttactgtattgtttatt.....tcatttgggtcttttggagtt 1222

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	52	4.3	7218	1	US-08-232-463-14
2	49.4	4.0	10467	4	US-10-204-708-2
3	48.8	4.0	19124	2	US-08-487-828B-13
4	45.8	3.7	936	4	US-09-328-352-1255
5	45.6	3.7	15016	4	US-09-601-198-60
6	45.2	3.7	53332	4	US-09-801-861-3
7	45	3.7	5152	4	US-10-204-708-73
8	44.8	3.7	5562	4	US-10-204-708-63
9	44.2	3.6	8961	4	US-10-204-708-80
10	44	3.6	5181	1	US-08-257-073-10
11	43.8	3.6	658	3	US-08-998-416-595
12	43.8	3.6	6156	4	US-10-204-708-60
13	43.4	3.6	10640	4	US-09-417-485D-5
14	42.6	3.5	6243	2	US-09-056-075-1
15	42.4	3.5	1563	4	US-09-508-370A-11
16	42.2	3.5	471	1	US-08-248-466B-5
17	42.2	3.5	1763	1	US-08-248-466B-2
18	42	3.4	1320	1	US-08-257-073-15
19	42	3.4	1482	3	US-08-098-327E-41
20	42	3.4	1482	3	US-08-098-327E-45
21	42	3.4	1482	4	US-08-462-625-41
22	42	3.4	1482	4	US-08-462-625-45
23	42	3.4	1493	3	US-08-098-327E-38
24	42	3.4	1493	4	US-08-462-625-38
25	42	3.4	4702	4	US-08-956-171B-268
26	41.8	3.4	6317	4	US-10-204-708-12
27	41.8	3.4	19513	4	US-10-204-708-40

C	28	41.6	3.4	4544	4	US-08-956-171E-517	Sequence 517, Appl
	29	41.6	3.4	5501	4	US-10-204-708-38	Sequence 38, Appl
C	30	41.4	3.4	2447	2	US-09-014-969-14	Sequence 14, Appl
	31	41.4	3.4	4818	3	US-08-817-926-27	Sequence 27, Appl
	32	41.4	3.4	5340	4	US-09-627-122-21	Sequence 21, Appl
	33	40.8	3.3	6583	4	US-10-204-708-26	Sequence 26, Appl
C	34	40.8	3.3	1664976	4	US-08-916-421B-1	Sequence 1, Appl
C	35	40.6	3.3	7218	1	US-08-232-463-14	Sequence 14, Appl
	36	40.6	3.3	19233	4	US-10-204-708-45	Sequence 45, Appl
	37	40.2	3.3	726	3	US-08-998-416-183	Sequence 183, Appl
C	38	40.2	3.3	1939	1	US-07-715-751B-2	Sequence 2, Appl
	39	40.2	3.3	6669	4	US-10-204-708-6	Sequence 6, Appl
	40	40.2	3.3	7295	2	US-08-487-826B-15	Sequence 15, Appl
C	41	39.8	3.3	240	1	US-08-628-417-6	Sequence 6, Appl
C	42	39.8	3.3	1051	3	US-09-245-041-10	Sequence 10, Appl
C	43	39.8	3.3	1696	4	US-09-835-811-1	Sequence 1, Appl
	44	39.8	3.3	6243	2	US-09-056-075-1	Sequence 1, Appl
C	45	39.8	3.3	640681	4	US-09-790-988-1	Sequence 1, Appl

ALIGNMENTS

RESULT 1
US-08-232-463-14
; Sequence 14, Application US/08232463
; Patent No. 5670367
; GENERAL INFORMATION:
; APPLICANT: DORNER, F.
; APPLICANT: SCHEIFLINGER, F.
; APPLICANT: FALKNER, F. G.
; TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
; NUMBER OF SEQUENCES: 52
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/08/232.463
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER: US/07/935.313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZgpt-Fls
US-08-232-463-14
Query Match 4.3%; Score 52; DB 1; Length 7218;


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; REFERENCE/DOCKET NUMBER: NIH121.001CPI
;
; TELECOMMUNICATION INFORMATION:
;
; TELEPHONE: (619) 235-8550
;
; TELEFAX: (619) 235-0176
;
; INFORMATION FOR SEQ ID NO: 13:
;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 19124 base pairs
;
; TYPE: nucleic acid
;
; STRANDEDNESS: single
;
; TOPOLOGY: linear
;
; MOLECULE TYPE: cDNA
;
; HYPOTHEetical: NO
;
; ANTI-SENSE: NO
;
; US-08-487-826B-13

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	Query Match	4.0%;	Score 48.8;	DB 2;	Length 19124;
	Best Local Similarity	48.0%;	Pred. No. 0.019;		
	Matches 169;	Conservative 0;	Mismatches 182;	Indels 1;	Gaps 1;
QY	841	T T T A A A T G A T T T T T T A B A A T A A G T A T A A A C T T T T T T A G A A C T A T C T C A T T T A A T T G A T	900		
Dd	15985	T G T A T A T G C A T G T A A T T A T T T A T T T T T T T T T T T A T T T T A A T T A A A T T T T T T T A T T	15926		
QY	901	A G T A C G T A A G G T T T A C A T C A T T A G G A G T A C T T G T T G A G C A A T C A T C A C T C G T T A C T G T	960		
Dd	15925	T T T T T T T A T T C A T A A A A T T T T T T T A A T T T T T T T T T T T A T T A A T T A A A T T T T T T A T T A T	15866		
QY	961	G A T G G T C A A C T A C C C A T A T G A A A T A T T T T T T A T A G T C C C A T C C T C G A A A G T A A T C C A C A	1020		
Dd	15865	T A T T T T T T T T A T T T A - A T T A A A T T T T T T T A T T A T T A T T T T T T T T T T A T T A A A T A A A A T T	15807		
QY	1021	T A T C A C A G T C T A T T A A T C T G A T C C T T C U T C A U C A A A T G T A A T T T C C T T T T T T T G G C G G	1080		
Dd	15806	T T T T T T A T T T A T G T A T A T T T T T T T T T T A C A T T T T T T A A T T T T T T T T T T T A T T T T A T T T A T G	15747		
QY	1081	T A T C C A T A C T G T T A A T G A A T G T T T T T A A T T C A T C T G T T T T T T C T G A G A A G A T A T C C T T T T	1140		
Dd	15746	A T A T A T A T T T T T A T T T A T A T A T T T T T T T C T T T T T T T T T T T G T T T T A T G A T A T A T A T T	15687		
QY	1141	T T G T T T T A A T G A C T C G A C A T G T A T A C T T T T A T T T C T T G T T T T C C T A A A A	1192		
Dd	15686	T T T T T T T T T T A A T G T T T T T T T T T T T T T T T T C T T T G T T T T A T T T T T T T T T A T A A A T A A A	15635		

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RESULT 4
US-09-328-352-1255
; Sequence 1255, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 1255
; LENGTH: 936
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-1255

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	Query Match	3.7%	Score 45.8;	DB 4;	Length 936;
	Best Local Similarity	47.4%;	Pred. No. 0.037;		
	Matches 137;	Conservative 0;	Mismatches 152;	Indels 0;	Gaps 0
Qy	157	TGTTATCTTTTGGAGACGTGAAGAGGACCTATTTTAGTAGATACAGGTATGCCAAGAGT	216		
Db	223	TGTCCTTTTGTGTAGAAACTGATCGAGGCCCTTGCTACTGATTGATACCGGATTTGGCCTACAA	282		
Qy	217	GCAGTTAAATATGAAGGTCTTTTTTAAACGGTACATTTGTCGAAGGGCAGGTTTTTACCGAAA	276		
Db	283	GATTATCTTACACATGCAACAGCGCCCTTGGCTCTTTTAGTCAACCGTTGGGGAAAAATTGAA	342		

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QY      277  ATGACTGAGAGATAGAAATCGTGAATATATTTAAACGCGGTTGGTTATGACCGCGAAGAC 336
Db      343  CCGAATCTTTGAGTTTCAGTCTGCTATTCAACAAATTCAGAAACTCGGTTTCCATCCTAAAGAT 402
QY      337  CTTCCTTTATATTATTAAGTTCTCACITTCGACTTTTGGATCATGCAGGAGGAAATGGCGCTTTT 396
Db      403  GTGCAGCACATTTTGTGACTCACCTCGACTTTGACCATGCAGCGGGAATTTCAGACTTT 462
QY      397  ATAAATACCAATCAATTTAGACGCGTGTGTAATATGAGCGCGCGGAGC 445
Db      463  CCCACGCCACTGTCCATGTGTAGTACTGAATACATGTGTGCGCAAC 511

RESULT 5
US-09-601-198-60
; Sequence 60, Application US/09601198
; Patent No. 6531583
; GENERAL INFORMATION:
; APPLICANT: Cassell, Gail H.
; APPLICANT: Chen, Ellison Y.
; APPLICANT: Glass, Jennifer S.
; APPLICANT: Glass, John I.
; APPLICANT: Heiner, Cheryl R.
; APPLICANT: Lefkowitz, Elliot
; TITLE OF INVENTION: NUCLEIC ACID PROBES AND METHOD FOR DETECTING UREAPLASMA
; TITLE OF INVENTION: UREALYTICUM
; FILE REFERENCE: UAB-13452/22
; CURRENT APPLICATION NUMBER: US/09/601,198
; CURRENT FILING DATE: 2000-12-08
; PRIOR APPLICATION NUMBER: 60/073,189
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 181
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 60
; LENGTH: 15016
; TYPE: DNA
; ORGANISM: Ureaplasma urealyticum
US-09-601-198-60

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Query Match	3.7%	Score 45.6	DB 4	Length 15016
Best Local Similarity	47.5%	Pred. No. 0.11		
Matches 172	Conservative 0	Mismatches 184	Indels 6	Gaps 1
Qy	786	CCCTGAATATATATAGTACAAAAGTCATGAGCTTATTGCTCATGACCTTTTTCGTTTAA	845	
Db	14646	CCGAGATCAACTTCATTATTTAAATGTTTTAACTGAAATTATCAACATCATCTGAACATAA	14705	
Qy	846	ATGATTTTTTTTAAATAAGTTATAAACTTTTTTTAGAACTATCTTCAATTAATGATGATGAC	905	
Db	14706	ATTGTTCTTTTGAAGATGTGATTCATCTTCTATGCTAAATGAAATCAAAATGATAAAATC	14765	
Qy	906	GTAAGGTTTACATCATTAGGAGTACTTCTGTGAGCAATCATCACTTCGTACTGTGATGG	965	
Db	14766	TTATCTTTTTGTAAAAATAGGGTGTGTGATAGATCAAAATGTGTGGTGTATTATTA	14825	
Qy	966	TCAACTACCCATCATGAAATATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCA	1025	
Db	14826	ACAAATTCGAGGAATTTTTATCAAAATACCATCAACATCTTGTAATTAACAAAAACGTCT	14885	
Qy	1026	CAGTCTATTAAATCTGATCCCTTCCTCATCTAAATGTTAAT-----TTTCCCTTTTGGGG	1079	
Db	14886	TGCGCTCTTCAACATTTTTTTTGGGCATCATCAAAACATAATGGTTATTAAACAAATTTACCA	14945	
Qy	1080	GTATCCATACCTGTTAATGAATCTTTTTTAATTCATCTGTTTTTGTGAGAAAGATATCCCTTT	1139	
Db	14946	ATATTAGTTTGTGTAACAATAATTTGTTTTTGGATCCAAATCAGCAACATTAAATACITTT	15005	
Qy	1140	TT 1141		
Db	15006	TT 15007		

RESULT 6

US-09-801-861-3
; Sequence 3, Application US/09801861
; Patent No. 6492154
; GENERAL INFORMATION:
; APPLICANT: YAN, Chunhua et al.
; TITLE OF INVENTION: ISOLATED HUMAN KINASE PROTEINS, NUCLEIC
; TITLE OF INVENTION: ACID MOLECULES ENCODING HUMAN KINASE PROTEINS, AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CL001098
; CURRENT APPLICATION NUMBER: US/09/801,861
; CURRENT FILING DATE: 2001-03-09
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 53332
; TYPE: DNA
; ORGANISM: Human
US-09-801-861-3

Query Match 3.7%; Score 45.2; DB 4; Length 53332;
Best Local Similarity 46.2%; Pred. No. 0.2;
Matches 184; Conservative 0; Mismatches 213; Indels 1; Gaps 1;

QY 797 TATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAATGATTTT 856
Db TTTAATAATAATTCCTAAAATGGCAATCAGTATATATTTTATATATATATATATAT 31340

QY 857 AAATAAGCTTATAAACTTTTATAGAACATCTCTCAATTTAAATGATGACGTTTAC 916
Db ATATTTTATATATATTTATATAGTATATATATATATATATATATATATATATAT 31341

QY 917 ATCAATGAGGATATCTTGTGAGCAATCACTCGCTGATGAGTGGTCACTACCA 976
Db ATATTTCTATATATTTATATATATATATATATATATATATATATATATATATAT 31401

QY 977 TATGAAATATTTTATAAGTCCCATCTCGAAAGTAAATCCACATATACAGTCTAT 1036
Db TATTTTAT 31461

QY 1037 ATCTGATCTCTTCTCATCTAATGTTAAATTTTCCCTTTTGGCGGTATCCCATCTGTTTAA 1096
Db ATTAT 31520

QY 1097 GAATGTTTTTAATTCATCTGTTTTGTGAGAAAGATATCCTTTTGTGTTTAAATGATC 1156
Db ATATTTAT 31580

QY 1157 GACATGATATCTTTTATTTCTGTTTCTTAAAGAA 1194
Db TAT 31640

RESULT 7

US-10-204-708-73
; Sequence 73, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7

; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 98
; SEQ ID NO 73
; LENGTH: 5152
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-204-708-73

Query Match 3.7%; Score 45; DB 4; Length 5152;
Best Local Similarity 43.4%; Pred. No. 0.1;
Matches 255; Conservative 0; Mismatches 330; Indels 2; Gaps 1;

QY 604 GTATTATTACGATTGATGATCGATACGAAAGAGAAATTTGAAATGAGTCCCATTT 663
Db GTGATTTTAAAGTTAATTTAAATTAATATATATATATATATATATATATATATAT 3488

QY 664 GCGGGATTTCAGTACAGAAATAGCTTTTATCTCAATTAACGTTTAAAGAGTGTGAT- 722
Db TATTTTATAGTTTAAAGGAGATTTTATATTAATTTTAAATAAGAGTTGGAATAATC 3548

QY 723 -GAAAGAGAGCCGATTTCTTTGGACATGATATAGACGAGAAAGGGGATGTAAG 781
Db GTTTAAATAATTTTGAATTTTGTAAATGTAAGAAATAAGTAAATATAGTTTGTAGA 3608

QY 782 TGTTCCTGTAATATATATAGTACAAAAGTATGAGCTTATTCGCTCATGCTTTTTCGT 841
Db ATTAGAAATTTATAGTGTAGTGTGTTTAAATATATATATATATATATATATATAT 3668

QY 842 TTAATGATTTTTTAAATAAGTATTAAGCTTTTTTAAAGTATCTTCAATTAATGATA 901
Db AAAAATGGGAAAATTTTTTATAAATTAAGATGTGTTAAAGGAAATAGTTTAAATGAA 3728

QY 902 GTACGTAAAGTTTACATCATTTAGGAGTATCTTGTGAGCAATCATCATCTGTTACTGTG 961
Db ATATTTTATTTTAAATTTTAGTGTAAAGAAATGATTTTAAATGTTGCTGTAATAA 3788

QY 962 ATGTCACATCCCATATAGAAATATTTTTTAAAGTCCCATCCCTCGAAAGTAAATCCCAT 1021
Db ATTGTATATATATATTTTGAATTTAAATAAGTTAAATTTTAAATAATATAAAATATA 3848

QY 1022 ATCACGCTCTTAAATCTGATCTCTCATCTAATGTTAAATTTTCTTTTGGCGGT 1081
Db AATAAAAAATTTTAAAGTATTTTTTAAATAAGTATATATATATATATATATATATAT 3908

QY 1082 ATCCATCTGTTAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCTTTT 1141
Db GTTATTTTATTTTAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTAT 3968

QY 1142 TGTTTTAAATGACTCGACATGATATCTTTTATTTCTTGTTCCTTA 1188
Db TTTTCTGTTAGGTGAAATGATAGTGGCTAAATACGGTTTATGATA 4028

RESULT 8

US-10-204-708-63
; Sequence 63, Application US/10204708
; Patent No. 6677731
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA Replication
; TITLE OF INVENTION: by Assessing DNA Methylation
; FILE REFERENCE: 5013.1012
; CURRENT APPLICATION NUMBER: US/10/204,708
; CURRENT FILING DATE: 2003-05-06
; PRIOR APPLICATION NUMBER: PCT/EP01/03971
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8

FILING DATE: 09-JUN-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/075,783
 FILING DATE: 11-JUN-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/852,305
 FILING DATE: 18-MAR-1992
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/672,183
 FILING DATE: 20-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Frommer, William S.
 REGISTRATION NUMBER: 25,506
 REFERENCE/DOCKET NUMBER: 454310-2570
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 840-3333
 TELEFAX: (212) 840-0712
 TELEX: 425066 CURTMS
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5181 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-257-073-10


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;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/056,075
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27386
; REFERENCE/DOCKET NUMBER: 960296.95238
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6243 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 3770..4013
; OTHER INFORMATION: /note= "RP4 origin of DNA transfer (orit) from
; OTHER INFORMATION: plasmid RP4"
;
; US-09-056-075-1
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Query Match 3.5%; Score 42.6; DB 2; Length 6243;
Best Local Similarity 50.2%; Pred. No. 0.43; Mismatches 104; Indels 0; Gaps 0;
Matches 105; Conservative 0;

QY 981 AATATATTTTATAGTCCCATCTCGAAGTAATCCACATATCACAGTCTATTAAATCT 1040
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1436 AAAAAATTTTTCAACTTTTAAATAAAATAATTTTATATTTTATTTTATTTT 1377
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1041 GATCCTTCTTCACTAAATGTTAAATTTCCCTTTTGGGGGTATCCATCTGTTAAATGAAT 1100
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1376 TATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATA 1317
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1101 GTTTTAAATTCATCTGTTTGTGAGAAAGATATCCCTTTTGTGTTTAAATTTGACTCGACA 1160
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1316 TTTTATTTTATTTATATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1257
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1161 TGTATATCTTTTATTTCTTTGTTTCCCTAA 1189
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1256 TTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 1228
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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RESULT 15
US-09-508-370A-11/c
; Sequence 11, Application US/09508370A
; Patent No. 6492131
; GENERAL INFORMATION:
; APPLICANT: Dieter Soll
; TITLE OF INVENTION: Class I-type Lysyl-tRNA Synthetase
; FILE REFERENCE: OCR-896
; CURRENT APPLICATION NUMBER: US/09/508,370A
; CURRENT FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: PCT/US98/18968
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: MS Dos
; SEQ ID NO 11
; LENGTH: 1563
; TYPE: DNA
; ORGANISM: Borrelia burgdorferi
; FEATURE:
; NAME/KEY: lysyl t-RNA synthetase
; OTHER INFORMATION: clone described in Example 3
;
; US-09-508-370A-11
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Query Match 3.5%; Score 42.4; DB 4; Length 1563;
Best Local Similarity 50.8%; Pred. No. 0.3;
Matches 127; Conservative 0; Mismatches 121; Indels 2; Gaps 1;
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QY 945 ATCACTTCGTTACTGTGATGGTCAACTACCCATATGAAATATTTTATTAAGTCCCATCC 1004
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1257 ATCTCTTATCCAAATTAATTCGCCAATTAATTTATTTATTTAGTTTGTCTTTTGACTTC 1198
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1005 TCGAAAGTAATCCACATATCACAGTCTCTATTAAATCTGATCCCTTCTTCATCTAAATGTTAAT 1064
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1197 TTGACGTTTTTCAAGTAATTTAAATTTTATTTATATTTTCAAATATTTGACTGAT 1138
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1065 TTTCCCTTTTGGGGGTATCCATCTGTTAAATGAAATGTTTTTAAATTCATCTGTTTGTG 1124
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1137 TACACTTAAATGTCGAAATCCGACCTGATAAGGGAATCTTTTGGCTGGCATGATGGTTG 1078
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1125 AGAAGATATCCCTTTTGTGTTTAAATTTGACTCGACATGATATCTTTTATTTCTTTGTTT 1184
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1077 AGATAGT--TCGTAATTCCTTTTAAATGCTCTTTTCTTTCTTTTACATCTCTACT 1020
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1185 CCTAAAAAGA 1194
Db ||||| |||||
QY 1019 CCATAGTAGA 1010
Db ||||| |||||
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Search completed: February 24, 2004, 04:24:23
Job time : 98 secs

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:22:42 : Search time 35 Seconds
(without alignments)
1843.233 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLYFVPAGRCMLDHS.....VFFGHDIQERGCKVFPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL 23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1315	100.0	250	2	Q9L8R8	Q9L8R8 bacillus sp
2	1280	97.3	250	2	Q8KWS6	Q8KWS6 bacillus sp
3	1270	96.6	250	2	Q8KTW5	Q8KTW5 bacillus th
4	1256	95.5	250	2	Q8KNY1	Q8KNY1 uncultured
5	1244	94.6	250	2	Q8RPW5	Q8RPW5 bacillus th
6	1230	93.5	250	2	Q8KTW9	Q8KTW9 bacillus th
7	1230	93.5	250	2	Q8KI79	Q8KI79 bacillus th
8	1228	93.4	250	2	Q8RPW6	Q8RPW6 bacillus th
9	1227	93.3	250	2	Q8KTW6	Q8KTW6 bacillus th
10	1222	92.9	250	2	Q8KTW8	Q8KTW8 bacillus th
11	1220	92.8	250	2	Q8KTW3	Q8KTW3 bacillus ce
12	1219	92.7	250	2	Q8RPW9	Q8RPW9 bacillus sp
13	1216	92.5	250	2	Q8KTX1	Q8KTX1 bacillus th
14	1213	92.2	250	2	Q8RPW7	Q8RPW7 bacillus th
15	1212	92.2	250	2	Q8RJA0	Q8RJA0 bacillus th
16	1209	91.9	250	2	Q8RPW4	Q8RPW4 bacillus th

17	1208	91.9	250	2	Q8KTW4	Q8ktw4 bacillus th
18	1206	91.7	250	2	Q8KTX0	Q8ktx0 bacillus th
19	1202	91.4	250	2	Q8RPW8	Q8rpw8 bacillus th
20	1200	91.3	250	2	Q8RPW3	Q8rpw3 bacillus ce
21	1199	91.2	250	2	Q8KTW7	Q8ktw7 bacillus th
22	315	24.0	263	2	Q8VPD5	Q8vpd5 agrobacteri
23	312	23.7	263	16	Q8UKH0	Q8ukh0 agrobacteri
24	299.5	22.8	268	16	Q988B9	Q988b9 rhizobium l
25	299	22.7	256	2	Q9WMD3	Q9wmd3 agrobacteri
26	260	19.8	269	17	Q97Y13	Q97y13 sulfobius
27	256.5	19.5	253	2	Q8KXV8	Q8kxv8 rhizobium e
28	252	19.2	219	2	Q9RH58	Q9rh58 bradyrhizob
29	251	19.1	301	17	Q9HQ42	Q9hq42 halobacteri
30	242.5	18.4	262	17	Q28763	Q28763 archaeoglob
31	239.5	18.2	271	17	Q978V7	Q978v7 thermoplasm
32	236	17.9	271	16	Q9RXY2	Q9rxy2 deinococcus
33	233.5	17.8	276	16	Q8U664	Q8u664 agrobacteri
34	210	16.0	279	16	Q9PDL8	Q9pdl8 xylella fas
35	195	14.8	136	16	Q8XS86	Q8xs86 ralstonia s
36	192.5	14.6	328	17	Q97CB9	Q97cb9 thermoplasm
37	188	14.3	285	16	Q8F9T6	Q8f9t6 leptospira
38	186	14.1	253	16	Q9RTE2	Q9rte2 deinococcus
39	185.5	14.1	261	17	Q9HLW9	Q9hlw9 thermoplasm
40	185.5	14.1	280	16	Q8NW27	Q8nw27 staphylococ
41	183.5	14.0	280	16	Q99TB7	Q99tb7 staphylococ
42	181.5	13.8	331	2	Q9ALW1	Q9alw1 plesiomonas
43	178.5	13.6	326	16	Q92RT6	Q92rt6 rhizobium m
44	176.5	13.4	321	16	Q8P8H8	Q8p8h8 xanthomonas
45	174.5	13.3	341	2	Q93SP1	Q93sp1 plesiomonas

ALIGNMENTS

RESULT 1

Q9L8R8 ID Q9L8R8 PRELIMINARY; PRT; 250 AA.
AC Q9L8R8;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative metallohydrolase.
GN AIIA.
OS Bacillus sp. 240B1.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=118641;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=240B1,
RX MEDLINE=20202669; PubMed=10716724;
RA Dong Y.H., Xu J.L., Li X.Z., Zhang L.H.;
RT "AIIA, an enzyme that inactivates the acylhomoserine lactone quorum-
sensing signal and attenuates the virulence of *Erwinia carotovora*.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:3526-3531(2000).
DR EMBL; AF196486; AAF62398.1; -;
DR InterPro; IPR001279; Bactmase-like.
DR Pfam; PF00753; lactamase_B; 1.
KW Hydrolase.
SQ SEQUENCE 250 AA; 28037 MW; 6E5D32E1E8818272 CRC64;

Query Match 100.0%; Score 1315; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 5.9e-105;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MTVKLYFVPAGRCMLDHSVNSTLTPGELLDLPVWCYLLETEEGPILVDVTGMPESAVNN	60
Db	1	MTVKLYFVPAGRCMLDHSVNSTLTPGELLDLPVWCYLLETEEGPILVDVTGMPESAVNN	60
QY	61	EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP	120
Db	61	EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP	120
QY	121	IIVQRAEYAAQHSEYKLCILPNLNKYIIEGDYEVWPGVQLLHTFGHTPGHQSLLIET	180

Db	121	IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET	180	OS	Bacillus thuringiensis serovar toumanoffi.
Qy	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OX	NCBI_TaxID=180862;
Qy	241	RGCKVPEPEYI 250		RN	SEQUENCE FROM N.A.
Db	241	RGCKVPEPEYI 250		RP	STRAIN=HD201;
				RX	MEDLINE=22142036; PubMed=12147491;
				RA	Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
				RT	"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
				RL	Widespread in Many Subspecies of Bacillus thuringiensis.";
				DR	EMBL; AF478058; AAM92139.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
					Query Match 96.6%; Score 1270; DB 2; Length 250;
					Best Local Similarity 96.0%; Pred. No. 4.e-101;
					Matches 240; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Db	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Qy	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Db	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Qy	181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Db	181 ENSGPVLLITDASYTKENFENEPVFPAGFDPPELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Qy	241 RGCKVPEPEYI 250
				Db	241 KGCKVPEPEYI 250
					RESULT 4
				ID	Q8KNV1 PRELIMINARY; PRT; 250 AA.
				AC	Q8KNV1; 2002 (TrEMBLrel. 22, Created)
				DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
				DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
				DE	N-acylhomoserine lactone lactonase.
				GN	Al12
				OS	uncultured Bacillus sp.
				OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
				OX	NCBI_TaxID=83428;
				RN	SEQUENCE FROM N.A.
				RA	Frav R.G., Dessaux Y.;
				RT	"Isolation of HSL lactonases and comparison of their activity against
				RL	various N-acylhomoserine lactone targets.";
				DR	EMBL; AJ505742; CAD44268.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28179 MW; E045D41BDAA659EA CRC64;
					Query Match 95.5%; Score 1256; DB 2; Length 250;
					Best Local Similarity 95.2%; Pred. No. 7e-100;
					Matches 238; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

Db	121	IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET	180	OS	Bacillus thuringiensis serovar toumanoffi.
Qy	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OX	NCBI_TaxID=180862;
Qy	241	RGCKVPEPEYI 250		RN	SEQUENCE FROM N.A.
Db	241	RGCKVPEPEYI 250		RP	STRAIN=HD201;
				RX	MEDLINE=22142036; PubMed=12147491;
				RA	Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
				RT	"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
				RL	Widespread in Many Subspecies of Bacillus thuringiensis.";
				DR	EMBL; AF478058; AAM92139.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
					Query Match 96.6%; Score 1270; DB 2; Length 250;
					Best Local Similarity 96.0%; Pred. No. 4.e-101;
					Matches 240; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Db	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Qy	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Db	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Qy	181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Db	181 ENSGPVLLITDASYTKENFENEPVFPAGFDPPELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Qy	241 RGCKVPEPEYI 250
				Db	241 KGCKVPEPEYI 250
					RESULT 4
				ID	Q8KNV1 PRELIMINARY; PRT; 250 AA.
				AC	Q8KNV1; 2002 (TrEMBLrel. 22, Created)
				DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
				DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
				DE	N-acylhomoserine lactone lactonase.
				GN	Al12
				OS	uncultured Bacillus sp.
				OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
				OX	NCBI_TaxID=83428;
				RN	SEQUENCE FROM N.A.
				RA	Frav R.G., Dessaux Y.;
				RT	"Isolation of HSL lactonases and comparison of their activity against
				RL	various N-acylhomoserine lactone targets.";
				DR	EMBL; AJ505742; CAD44268.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28179 MW; E045D41BDAA659EA CRC64;
					Query Match 95.5%; Score 1256; DB 2; Length 250;
					Best Local Similarity 95.2%; Pred. No. 7e-100;
					Matches 238; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

Db	121	IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET	180	OS	Bacillus thuringiensis serovar toumanoffi.
Qy	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OX	NCBI_TaxID=180862;
Qy	241	RGCKVPEPEYI 250		RN	SEQUENCE FROM N.A.
Db	241	RGCKVPEPEYI 250		RP	STRAIN=HD201;
				RX	MEDLINE=22142036; PubMed=12147491;
				RA	Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
				RT	"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
				RL	Widespread in Many Subspecies of Bacillus thuringiensis.";
				DR	EMBL; AF478058; AAM92139.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
					Query Match 96.6%; Score 1270; DB 2; Length 250;
					Best Local Similarity 96.0%; Pred. No. 4.e-101;
					Matches 240; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Db	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Qy	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Db	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Qy	181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Db	181 ENSGPVLLITDASYTKENFENEPVFPAGFDPPELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Qy	241 RGCKVPEPEYI 250
				Db	241 KGCKVPEPEYI 250
					RESULT 4
				ID	Q8KNV1 PRELIMINARY; PRT; 250 AA.
				AC	Q8KNV1; 2002 (TrEMBLrel. 22, Created)
				DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
				DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
				DE	N-acylhomoserine lactone lactonase.
				GN	Al12
				OS	uncultured Bacillus sp.
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				RN	SEQUENCE FROM N.A.
				RA	Frav R.G., Dessaux Y.;
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				DR	EMBL; AJ505742; CAD44268.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28179 MW; E045D41BDAA659EA CRC64;
					Query Match 95.5%; Score 1256; DB 2; Length 250;
					Best Local Similarity 95.2%; Pred. No. 7e-100;
					Matches 238; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

Db	121	IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET	180	OS	Bacillus thuringiensis serovar toumanoffi.
Qy	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OX	NCBI_TaxID=180862;
Qy	241	RGCKVPEPEYI 250		RN	SEQUENCE FROM N.A.
Db	241	RGCKVPEPEYI 250		RP	STRAIN=HD201;
				RX	MEDLINE=22142036; PubMed=12147491;
				RA	Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
				RT	"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
				RL	Widespread in Many Subspecies of Bacillus thuringiensis.";
				DR	EMBL; AF478058; AAM92139.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
					Query Match 96.6%; Score 1270; DB 2; Length 250;
					Best Local Similarity 96.0%; Pred. No. 4.e-101;
					Matches 240; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Db	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
				Qy	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Db	121 IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET 180
				Qy	181 EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Db	181 ENSGPVLLITDASYTKENFENEPVFPAGFDPPELALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
				Qy	241 RGCKVPEPEYI 250
				Db	241 KGCKVPEPEYI 250
					RESULT 4
				ID	Q8KNV1 PRELIMINARY; PRT; 250 AA.
				AC	Q8KNV1; 2002 (TrEMBLrel. 22, Created)
				DT	01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
				DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
				DE	N-acylhomoserine lactone lactonase.
				GN	Al12
				OS	uncultured Bacillus sp.
				OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
				OX	NCBI_TaxID=83428;
				RN	SEQUENCE FROM N.A.
				RA	Frav R.G., Dessaux Y.;
				RT	"Isolation of HSL lactonases and comparison of their activity against
				RL	various N-acylhomoserine lactone targets.";
				DR	EMBL; AJ505742; CAD44268.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28179 MW; E045D41BDAA659EA CRC64;
					Query Match 95.5%; Score 1256; DB 2; Length 250;
					Best Local Similarity 95.2%; Pred. No. 7e-100;
					Matches 238; Conservative 5; Mismatches 7; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Qy	61 EGLFNGTFVEGQVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

Db	121	IIIVORAEYAAQHSSEYLVKCEILPNLNKYIIEGDYVVPVGVQVLLHTPGHTPGHQSLLIET	180	OS	Bacillus thuringiensis serovar toumanoffi.
Qy	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Db	181	EKSGPVLITDASYTKENFENEPVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ	240	OX	NCBI_TaxID=180862;
Qy	241	RGCKVPEPEYI 250		RN	SEQUENCE FROM N.A.
Db	241	RGCKVPEPEYI 250		RP	STRAIN=HD201;
				RX	MEDLINE=22142036; PubMed=12147491;
				RA	Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
				RT	"Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
				RL	Widespread in Many Subspecies of Bacillus thuringiensis.";
				DR	EMBL; AF478058; AAM92139.1;
				DR	InterPro; IPR001279; Blactmase-like.
				DR	Pfam; PF00753; lactamase_B; 1.
				SQ	SEQUENCE 250 AA; 28080 MW; 3188759211697975 CRC64;
					Query Match 96.6%; Score 1270; DB 2; Length 250;
					Best Local Similarity 96.0%; Pred. No. 4.e-101;
					Matches 240; Conservative 6; Mismatches 4; Indels 0; Gaps 0;
				Qy	1 MTVKKLYFVPAGRCMLDHSVNSTLTGCLLDLPVWCYLLTEEGPILVDVTGMPESAVNN 60
				Db	1 MTVKKLYFVPAGRCMLDHS

DR Pfam: PF00753; lactamase_B; 1. 1B9DC273F9CB15CF CRC64;
SQ SEQUENCE 250 AA; 28121 MW; 1B9DC273F9CB15CF CRC64;

Query Match 93.5%; Score 1230; DB 2; Length 250;
Best Local Similarity 91.2%; Pred. No. 1.2e-97;
Matches 228; Conservative 15; Mismatches 7; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETETEGPILVDTGMPESAVNN 60
DB 1 MTVKLYFVPAGRCMLDSSVNSTLTPGNLLNLPVWCYLLETETEGPILVDTGMPESAVNN 60

QY 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120
DB 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120

QY 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180
DB 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180

QY 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240

QY 241 RGCKVPPEYI 250
DB 241 KGCKVPPEYI 250

RESULT 8
Q8RPW6 PRELIMINARY; PRT; 250 AA.

ID Q8RPW6
AC Q8RPW6
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-OCT-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE AHL-Lactonase.
GN AIIA-B17.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=B17;
RX MEDLINE=21914084; PubMed=11916693;
RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
RT Bacillus Species.";
RL Appl. Environ. Microbiol. 68:1754-1759(2002).
DR EMBL: AF350930; AAL98719.1; -;
DR InterPro: IPR001279; Blactmase-like.
DR Pfam: PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28163 MW; 12A78D220E1B2DD0 CRC64;

Query Match 93.4%; Score 1228; DB 2; Length 250;
Best Local Similarity 92.8%; Pred. No. 1.8e-97;
Matches 232; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETETEGPILVDTGMPESAVNN 60
DB 1 MTVKLYFVPAGRCMLDSSVNSTLTPGNLLNLPVWCYLLETETEGPILVDTGMPESAVNN 60

QY 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120
DB 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120

QY 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180
DB 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180

QY 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240

QY 241 RGCKVPPEYI 250
DB 241 KGCKVPPEYI 250

RESULT 9
Q8KTW6 PRELIMINARY; PRT; 250 AA.

ID Q8KTW6
AC Q8KTW6
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AIIA-like protein.
GN AIIA.
OS Bacillus thuringiensis serovar entomocidus/subtoxius.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180853;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HD109;
RX MEDLINE=22142036; PubMed=12147491;
RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
RT "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
RT Widespread in Many Subspecies of Bacillus thuringiensis.";
RL Appl. Environ. Microbiol. 68:3919-3924(2002).
DR EMBL: AF478056; AAM92137.1; -;
DR InterPro: IPR001279; Blactmase-like.
DR Pfam: PF00753; lactamase_B; 1.
SQ SEQUENCE 250 AA; 28101 MW; 8DE872267E3DAD2D CRC64;

Query Match 93.3%; Score 1227; DB 2; Length 250;
Best Local Similarity 91.6%; Pred. No. 2.2e-97;
Matches 229; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETETEGPILVDTGMPESAVNN 60
DB 1 MTVKLYFVPAGRCMLDSSVNSTLTPGNLLNLPVWCYLLETETEGPILVDTGMPESAVNN 60

QY 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120
DB 61 EGLFNGTFVEGOVLPMKTEEDRVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNTNP 120

QY 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180
DB 121 IIVQRAEYEAQHSSEYLKCEILPNLNKYKIEGDYEVVPGVQLLHPTPGHQSLLIET 180

QY 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLITDASYTKENFENFVFPAGFDSFELALSSIKRLKEVVMKEKPIVFFGHDIQE 240

QY 241 RGCKVPPEYI 250
DB 241 KGCKVPPEYI 250

RESULT 10
Q8KTW8 PRELIMINARY; PRT; 250 AA.

ID Q8KTW8
AC Q8KTW8
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE AIIA-like protein.
GN AIIA.
OS Bacillus thuringiensis serovar ostrinae.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=180883;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=HD501;
RX MEDLINE=22142036; PubMed=12147491;
RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
RT "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are

RT Widespread in Many Subspecies of *Bacillus thuringiensis*.;
 RL Appl. Environ. Microbiol. 68:3919-3924(2002).
 DR EMBL; AF478054; AAM92135.1; -;
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28163 MW; BA2D7F09CF3F39DD CRC64;

Query Match 92.9%; Score 1222; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 5.8e-97;
 Matches 228; Conservative 14; Mismatches 8; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAGRCMLDHSVNSLTTPGELLDLVPCVLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKLYFIPAGRCMLDHSVNSLTTPGKLLNLPVWCYLLTEEGPILVDTGMPESAVNN 60
 Qy 61 EGLFNGTFVEGOVLPMKTEEDRIIVNLRKVGYPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGOVLPMKTEEDRIIVNLRKVGYPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGLLHTPGHTPGHOSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLNKYIIEGDEYVVPVGLLHTPGHOSLLIET 180
 Qy 181 EKSGPVLTTIDASTYKTNFENVPFAGFDSSELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Db 181 EQSGSVLLTTIDASTYKTNFENVPFAGFDPPELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCRVFPEYI 250

RESULT 11

Q8KWT3 PRELIMINARY; PRT; 250 AA.

ID Q8KWT3
 AC Q8KWT3;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE AiiA-like protein.
 GN AiiA.
 OS *Bacillus cereus*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1396;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IBN35;
 RX MEDLINE=22142036; PubMed=12147491;
 RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
 "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
 Widespread in Many Subspecies of *Bacillus thuringiensis*.";
 RL Appl. Environ. Microbiol. 68:3919-3924(2002).
 DR EMBL; AF478051; AAM92142.1; -;
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28113 MW; DFF28F553BA07C2E CRC64;

Query Match 92.8%; Score 1220; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 8.6e-97;
 Matches 228; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAGRCMLDHSVNSLTTPGELLDLVPCVLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKLYFIPAGRCMLDHSVNSLTTPGKLLNLPVWCYLLTEEGPILVDTGMPESAVNN 60
 Qy 61 EGLFNGTFVEGOVLPMKTEEDRIIVNLRKVGYPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGOVLPMKTEEDRIIVNLRKVGYPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGLLHTPGHTPGHOSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLNKYIIEGDEYVVPVGLLHTPGHOSLLIET 180

Qy 181 EKSGPVLTTIDASTYKTNFENVPFAGFDSSELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Db 181 EQSGSVLLTTIDASTYKTNFENVPFAGFDPPELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCRVFPEYI 250

RESULT 12

Q8RPW9 PRELIMINARY; PRT; 250 AA.

ID Q8RPW9
 AC Q8RPW9;
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE AHL-lactonase.
 GN AiiA-COT1.
 OS *Bacillus sp. COT1*.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=176903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=COT1;
 RX MEDLINE=21914084; PubMed=11916693;
 RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
 "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
 RT *Bacillus* Species.";
 RL Appl. Environ. Microbiol. 68:1754-1759(2002).
 DR EMBL; AF350927; AAL98716.1; -;
 DR InterPro; IPR001279; Blactmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 SQ SEQUENCE 250 AA; 28084 MW; 3508246790F50709 CRC64;

Query Match 92.7%; Score 1219; DB 2; Length 250;
 Best Local Similarity 91.2%; Pred. No. 1.1e-96;
 Matches 228; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

Qy 1 MTVKLYFVPAGRCMLDHSVNSLTTPGELLDLVPCVLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKLYFVPAGRCMLDHSVNSLTTPGKLLNLPVWCYLLTEEGPILVDTGMPESAVNN 60
 Qy 61 EGLFNGTFVEGOVLPMKTEEDRIIVNLRKVGYPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 ENLFEFTFAGQILPKMTEEDRIIALLKRAYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Qy 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGLLHTPGHTPGHOSLLIET 180
 Db 121 IIVQRAEYEAQHSEYLYKECILPNLNKYIIEGDEYVVPVGLLHTPGHTPGHOSLLIET 180
 Qy 181 EKSGPVLTTIDASTYKTNFENVPFAGFDSSELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Db 181 EKSGVLLTTIDASTYKTNFENVPFAGFDPPELALSSIKRLKEVVMKPKPIVFFGHDIQEQ 240
 Qy 241 RGCKVFPEYI 250
 Db 241 KGCRVFPEYI 250

RESULT 13

Q8KTX1 PRELIMINARY; PRT; 250 AA.

ID Q8KTX1
 AC Q8KTX1;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE AiiA-like protein.
 GN AiiA.
 OS *Bacillus thuringiensis* serovar canadensis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=180855;
 RN [1]
 RP SEQUENCE FROM N.A.

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RC STRAIN=HD224;
RX MEDLINE=22142036; PubMed=12147491;
RA Lee S.J., Park S.Y., Lee J.J., Yum D.Y., Koo B.T., Lee J.K.;
RT "Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
RT Widespread in Many Subspecies of Bacillus thuringiensis.";
RL Appl. Environ. Microbiol. 68:3919-3924(2002).
DR EMBL; AF478047; AM92128.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase B; 1.
SQ SEQUENCE 250 AA; 28003 MW; 6EB53AF4A152B244 CRC64;

Query Match 92.5%; Score 1216; DB 2; Length 250;
Best Local Similarity 91.2%; Pred. No. 1.9e-96;
Matches 228; Conservative 12; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
Db 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
QY 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

RESULT 14
Q8RPW7 ID Q8RPW7 PRELIMINARY; PRT; 250 AA.
AC Q8RPW7;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE AHL-lactonase (Aila-like protein).
GN Aila-B2 OR Aila.
OS Bacillus thuringiensis,
OS Bacillus thuringiensis (subsp. aizawai),
OS Bacillus thuringiensis (subsp. kurstaki), and
OS Bacillus thuringiensis serovar indiana.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428, 1433, 29339, 180850;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=B.thuringiensis; STRAIN=B2;
RX MEDLINE=21914084; PubMed=11916693;
RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
RT Bacillus Species.";
RL Appl. Environ. Microbiol. 68:1754-1759(2002).
DR EMBL; AF350934; AAL98723.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase B; 1.
SQ SEQUENCE 250 AA; 28004 MW; 6055D4F4A152B244 CRC64;

Query Match 92.2%; Score 1212; DB 2; Length 250;
Best Local Similarity 90.8%; Pred. No. 4.2e-96;
Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
Db 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
QY 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

RESULT 15
Q8RJA0 ID Q8RJA0 PRELIMINARY; PRT; 250 AA.
AC Q8RJA0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE AHL-lactonase.
GN Aila-B20 OR Aila-B22.
OS Bacillus thuringiensis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1428;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=B20, and B22;
RX MEDLINE=21914084; PubMed=11916693;
RA Dong Y.H., Gusti A.R., Zhang Q., Xu J.L., Zhang L.H.;
RT "Identification of Quorum-Quenching N-Acyl Homoserine Lactonases from
RT Bacillus Species.";
RL Appl. Environ. Microbiol. 68:1754-1759(2002).
DR EMBL; AF350932; AAL98721.1; -.
DR EMBL; AF350934; AAL98723.1; -.
DR InterPro; IPR001279; Blactmase-like.
DR Pfam; PF00753; lactamase B; 1.
SQ SEQUENCE 250 AA; 28004 MW; 6055D4F4A152B244 CRC64;

Query Match 92.2%; Score 1212; DB 2; Length 250;
Best Local Similarity 90.8%; Pred. No. 4.2e-96;
Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
Db 1 MTVKLYFVPAGRCMLDSSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
QY 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
Db 61 EGLFNGTFFVEGQVLPKMTTEEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFNT 120
QY 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
Db 121 IIVQRAEYEAASHSEYKCEILPNLNYKIIEGDYEVVPGVQLLHTPGHSPGHSLFIET 180
QY 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
Db 181 EKSGPVLLTIDASYTKENFENVPFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
QY 241 RGCKVPPEYI 250
Db 241 KGCRVPPEYI 250

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QY 241 RGCKVFPEYI 250
: ||: |||||
Db 241 KGCRVFPEYI 250

Search completed: February 20, 2004, 16:26:00
Job time : 36 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 02:25:33 ; Search time 2464 Seconds

(without alignments)
14809.896 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgttttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_estl:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	75.8	6.2	1101	29	CNS0039G
2	74	6.1	576	29	CNS035N7
C 3	72.2	5.9	1165	13	AL228940 Tetraodon
4	72	5.9	1124	13	BX338369 BX338369
					BX436282 BX436282

5	58.6	5.6	1123	14	CD325190
C 6	67.6	5.5	1067	14	CD386564
7	67	5.5	1101	29	CNS0039G
C 8	67	5.5	1201	9	AL565455
C 9	66.8	5.5	1101	29	CNS00EVL
10	66.8	5.5	1201	13	BX335216
11	66.4	5.4	897	29	CNS07ABZ
C 12	66.4	5.4	1056	13	BX415058
C 13	66.2	5.4	1201	13	BX395112
C 14	66	5.4	981	13	BX425658
15	65.8	5.4	1200	13	BX436510
C 16	65.6	5.4	1201	13	BX357882
C 17	65.4	5.4	991	14	CD248081
C 18	64.8	5.3	1200	13	BX437758
19	64.4	5.3	739	14	CF217629
20	64.4	5.3	1101	29	CNS00EVL
21	64.4	5.3	1309	10	BE420736
C 22	63.8	5.2	1101	29	CNS003B4
C 23	63.4	5.2	1048	13	BX456942
24	63.2	5.2	1044	13	BX415231
25	63.2	5.2	1101	29	CNS001FB
26	62.8	5.1	756	28	AZ192623
C 27	62.8	5.1	974	29	CNS00ITT
C 28	62.6	5.1	1101	29	CNS002LJ
C 30	62.4	5.1	1126	13	BX446388
C 31	62.2	5.1	1184	29	CNS04P4P
C 32	62.2	5.1	1201	9	AL547503
33	62	5.1	1287	29	CG753143
34	61.6	5.0	922	28	AZ548363
C 35	61.4	5.0	1101	29	CNS003B0
36	61.2	5.0	717	29	CNS06ZNC
37	61.2	5.0	932	9	AL514901
C 38	61.2	5.0	953	13	BX331505
C 39	61.2	5.0	994	13	BX414650
C 40	61.2	5.0	1002	14	CD389396
C 41	61.2	5.0	1101	29	CNS00Z6Z
C 42	61.2	5.0	1159	13	BX341161
C 43	61	5.0	920	29	CNS01UQL
C 44	60.8	5.0	961	28	AZ691838
C 45	60.8	5.0	1101	29	CNS00LJT

ALIGNMENTS

RESULT 1

CNS0039G/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence.

AL063921

AL063921.1 GI:4941778

GSS.

Drosophila melanogaster (fruit fly)

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)

Genoscope.

Direct Submission

Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr

- Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a

collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila

melanogaster genome using these BACs. For further information

please see <http://www.fruitfly.org> The BDGP Drosophila

melanogaster BAC library was prepared by Kazutoyo Osoegawa and

Aaron Mammos in Pieter de Jong's laboratory in the Department of

Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain Y2; cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.

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FEATURES
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Best Local Similarity 18.7%; Pred. No. 2.5e-05;
Matches 162; Conservative 322; Mismatches 382; Indels 1; Gaps 1;

QY 219 AGTTAATAATCAAGGCTCTTTTAAACGGTACATTTGTCAAGGCGAGGCTTTTACCGAAAT 278
Db 1096 WGDWTDRDTRKDDWIKWTKWTKWRKDRADDERWAGDADRWADWDGAGTWTATWWW 1037
QY 279 GACTGAAGAAGATAGATTCGTGAATATTTTAAACGGGTTGGTTTATGAGCGCGAAGACCT 338
Db 1036 WATWDTWMDKWWWATAAKTDATWMTWRATWADWAGDRGAGKRDRDAATDADGAGRRD 977
QY 339 TCATTATATATAGTTCTCACTGCGATTTTGATTCATCCAGGAGGAATGCGGCTTTAT 398
Db 976 GGRKRDKDKDGGDDKGGKKKAAKAAKATWKKWDDWDDKWDWGDGAKRDRADDD 917
QY 399 AAATACACCAATCATTTACAGCGTGTGAATATGATGAGCGCGCAGCATACGAGAAATA 458
Db 916 GAGKDDGKGDADDDTDGTDKDDDKDDWDDKAGTWGDATWAAATDWWWGWADA 857
QY 459 TTTGAAAGAGATGATATTCGCGAATTTAAACATAAAATCATGAGGTGATTTAGAGT 518
Db 856 DWTTWDAADDDWADDDWADWAWKWDWADWAGARTADRRDWDGDRAGKRGARKERDRKA 797
QY 519 CGTACGAGGAGTTCAATTTATGTCATACACAGGCGCATCTCCAGGCGATCATCGCTATT 578
Db 796 DKRDAADDDDAATTTTGTCTTTRDDDDKWKTDWTRWAADRTWDRDDDDDDDRDAGTA 737
QY 579 AATTGAGACAGAAAATCCGGCTCTGTATTTAATCAAGCATTCATCGTATACGAAAGA 638
Db 736 GRKWRRTWKRWRKRDFTWDDADDDTARDERRRGDDGADGKGTGRKRRDRATW 677
QY 639 GAATTTGAAATGAAGTGCATTTGCGGATTTGATTTCAGAAATGAGCTTTATCTTCAAT 698
Db 676 DRDADWADAATWTTTDTDDDKRDRRRKRGARRRRTTARAADWMTWKAWDWAKWDW 617
QY 699 TAAAGCTTTAAAGAGTGTGATCAAGAGAGAGCGGATTTGTTCTTTGGACATGATAT 758
Db 616 KTRADRDWDAADTWDTRADRDWAKARAWARWRDRARAARDRRTWTKGTTTATWTT 557
QY 759 AGACGAGAAAGGCGATGTAAGTGTTCCTCTCAATATATATAGTACAAAAGTTCATGAGC 818
Db 556 WAARAAWWAWAATTTATWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTTWTWTTT 497
QY 819 TTATTCGCTCAGACTTTTCGTTTAAATGATTTTAAATAGTTTAAATAGTTTAAATAGTT 878
Db 496 AAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATA 437
QY 879 GAACATCTCTCATTTAAATTTGATGATGATGATGATGATGATGATGATGATGATGATG 938
Db 436 -TWTWTAATATTTTWTWTTTAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 378
QY 939 GCAATCATCATCTCGTCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 998
Db 377 CCCCTCCYCCCTCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCYCCY 318
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QY 999 CCATCTCGAAGTAATCCACATATCAGCTATTAAATCTGTATCTTCTTCTCATCTAAT 1058
Db 317 YYYCYCTCNMCNCCYCYCTTTCYCTTTCNMCNCCYCCYCYCYCYCYCYCYCYCYCCC 258
QY 1059 GTTAATTTCTCTTTTGGCGGTATCC 1085
Db 257 YYYCYCTTTCYCTTTCYCTTTCYCTTTCYCTTTCYCTTTCYCTTTCYCTTTCYCTTTC 231

RESULT 2
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LOCUS             Tetraodon nigroviridis genome survey sequence PUC-Ori end of clone
DEFINITION        214A06 of library G from Tetraodon nigroviridis, genomic survey
                    sequence.
ACCESSION         AL228940.1 GI:7887933
VERSION           AL228940.1
KEYWORDS          GSS; genome survey sequence.
SOURCE            Tetraodon nigroviridis
ORGANISM          Tetraodon nigroviridis
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                  Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
                  Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE         1 Roest Crolius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                  Saurin,W. and Weissenbach,J.
                  Estimate of human gene number provided by genome-wide analysis
                  using Tetraodon nigroviridis DNA sequence
                  Nat. Genet. 25 (2), 235-238 (2000)
                  20296633
                  PUBMED 10835645
REFERENCE         2 Roest Crolius,H., Jaillon,O., Dasilva,C., Ozouf-Costaz,C.,
                  Fizames,C., Fischer,C., Bouneau,L., Billault,A., Quetier,F.,
                  Saurin,W., Bernot,A. and Weissenbach,J.
                  Characterization and repeat analysis of the compact genome of the
                  freshwater pufferfish Tetraodon nigroviridis
                  Genome Res. 10 (7), 939-949 (2000)
                  20359837
                  PUBMED 10899143
REFERENCE         3 (bases 1 to 576)
                  Genoscope.
                  Direct Submission
                  Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
                  BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
                  - Web : www.genoscope.cns.fr)
                  This sequence is a single read and was generated as part of a large
                  scale clone-end sequencing project of the Tetraodon nigroviridis
                  genome. For more information, please take a look at
                  http://www.genoscope.cns.fr/Tetraodon.
                  Location/Qualifiers
FEATURES           1..576
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Query Match          6.1%; Score 74; DB 29; Length 576;
Best Local Similarity 42.1%; Pred. No. 6.7e-05;
Matches 191; Conservative 33; Mismatches 230; Indels 0; Gaps 0;

QY 737 TTGTTTCTTTGGACATCATATAGACGAGGAGGAGGATGTAAGTGTTCCTCGAATATA 796
Db 12 TTTTCTTTTGGATTTGGATTTGAAAAAATAAATAAATAAATAAATAAATAAATAAATAA 71
QY 797 TATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTTCGTTTAAATGATTTTTT 856
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AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
 Office of Cancer Genomics
 National Cancer Institute / NIH
 Bldg. 31 Rm10A07 Bethesda, MD 20892
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Jamie Thompson, University of WI
 cDNA Library Preparation: Gina Zastrow-Hayes
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (ILNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNL at:
<http://image.llnl.gov>
 Plate: NDKM74 row: e column: 02
 High quality sequence start: 8
 High quality sequence stop: 462.
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 LIBR PROVIDER - Bradfield"

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 Best Local Similarity 43.6%; Pred. No. 0.0011;
 Matches 265; Conservative 0; Mismatches 338; Indels 5; Gaps 1;
 582 TGACACAGAAAATCCGGTCCTGATTATTAAACGATTGATCGATCGTATACGAAAGAA 641
 926 TTAATATATAATATTTTAAATTTTATTTTAAATTTATATAAATTTTAAATATTA 867
 642 TTTTGAATAAGTGCATTTGCGGATTTGATTCAGAAATAGCTTTATCTCAATTA 701
 866 TGATATANNTTAAATTTTNNAAATTTTAAATTAANAATAATTTTNTATATA 807
 702 ACGTTTAAAGAGTGTGATGAAGAGAGCCGATTTCTTTCTGGACATGATAGA 761
 806 TAATATTATATAATTTTATTTANTTNATTTTAAATTTATTTTAAATATAAAT 747
 762 GCAGGAAGGGGATGTAAGTGTTCCTCGATATATATAGTACAAAAGTCATGAGCTTA 821
 746 ANANAAAAAATAAATAATTTTATTTATTTTAAATAAATAAATTTTAAAAAT 687
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 686 TAATTAATAAATAATATATTTTATTTTANATTATAATAATAATAATTTTATT 627
 882 CTATCTTCATTT-----AATGTAGTACGTAAAGTTTACATCATAGGAGTATCTGTT 936
 626 TTAATTTNANNTTTATAAATTTATTTTATATAAAAAAATAAATAATTTTAT 567
 937 GAGCAATCATCTCTGTTACTGTGATGGTCACTACCCATATCAATATTTTATAAG 996
 566 ABAATAAAAAAATTTATTTTNNAAAAAATAAATAAATAAATAAATTTTATTT 507
 997 TCCCATCTCGAAAGTAAATCCACATATACAGTCTATTAAATCTGATCTCTCATCTA 1056
 506 TTTNNCTCTTTNTTTTAAAAAANNNNNNNNNNTTTTATTTTATTTTATTTT 447
 1057 ATGTTAATTTTCCTTTTCGCGGTATCCATACGTGTAATGAATGTTTAAATCATCTG 1116
 446 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 387
 1117 TTTTGTGAGAAAGATATCTCTTTTTCGTTTAAITGACTCGACATGATATCTTTATTT 1176

Db 386 TTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTT 327
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 CNS0039G 1101 bp DNA linear GSS 03-JUN-1999
 Drosophila melanogaster genome survey sequence TET3 end of BAC #
 BACR08K10 of RPCI-98 library from Drosophila melanogaster (fruit
 fly), genomic survey sequence.
 AL063921
 AL063921.1 GI:4941778
 GSS.
 Drosophila melanogaster (fruit fly)
 Drosophila melanogaster
 Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 Ephydroidea; Drosophilidae; Drosophila.
 1 (bases 1 to 1101)
 Genoscope.
 Direct Submission
 Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 Determination of this BAC-end sequence was carried out as part of a
 collaboration with the Berkeley Drosophila Genome Project (BDGP).
 The BDGP is constructing a physical map of the Drosophila
 melanogaster genome using these BACs. For further information
 please see <http://www.fruitfly.org> The BDGP Drosophila
 melanogaster BAC library was prepared by Kazutoyo Osoegawa and
 Aaron Mammeter in Pieter de Jong's laboratory in the Department of
 Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
 NY. The library is named RPCI-98 and was constructed by partial
 EcoRI digestion of Drosophila DNA provided by the BDGP from the
 isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
 P1 and EST libraries. A more detailed description of the library
 and how to order individual BAC clones, the entire library, or
 filters for hybridization from the BACPAC Resource Center can be
 found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
FEATURES Location/Qualifiers
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ORIGIN

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 Best Local Similarity 19.3%; Pred. No. 0.0015;
 Matches 110; Conservative 221; Mismatches 234; Indels 0; Gaps 0;
 628 TATACGAAAGAGAAATTTTGAATAATGAAGTCCCATTTGCGGATTTGATTGAGAAATAGCT 687
 397 TATAAANNN 456
 688 TTAATCTCAATTAACCGTTTAAAGAGAGTGGTGGTGAAGAGAGCGGATTTGTTCTTT 747
 457 WAMTAWMTTATWTAATAAAAAAATAATTTTATTTTATTTTATTTTATTTTATTTT 516
 748 GGACATGATATACAGCAGGAGGAGGATGTAAGTGTTCCTCGAATATATATAGTACAA 807
 517 WAAAAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAAATAA 576
 808 AAGTCATGACTTATTCGCTCATGACTTTTTCGTTTAAATGATTTTATTTTAAATAGTAT 867
 577 TTYHYHYTY 636


```

- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a
collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila
melanogaster genome using these BACs. For further information
please see http://www.fruitfly.org The BDGP Drosophila
melanogaster BAC library was prepared by Kazutoyo Osoegawa and
Aaron Mammos in Pieter de Jong's laboratory in the Department of
Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
NY. The library is named RPCI-98 and was constructed by partial
EcoRI digestion of Drosophila DNA provided by the BDGP from the
isogenic strain Y2; cn bw sp, the same strain used for the BDGP's
p1 and EST libraries. A more detailed description of the library
and how to order individual BAC clones, the entire library, or
filters for hybridization from the BACPAC Resource Center can be
found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
Location/Qualifiers
1. .1101
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Best Local Similarity 35.1%; Pred. No. 0.0016;
Matches 209; Conservative 94; Mismatches 286; Indels 7; Gaps 2;
QY 591 AAAATCGGTCCTGATTATTAAAGATGATCGATCGATACGAAAGAGATTTTGA 650
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QY 651 TGAAGTCCCATTTCCGGGATTTGATTCAGAAATGAGCTTTATCTTCAATTAACGTTTAAA 710
DB 1008 ATATATWTATATATATATATATATATATATATATATATATATATATATAT 949
QY 711 AGAAGTGGTATGAAGAGAGACCGATTTGTTTCTTGGACATGATATAGAGAGGAAAG 770
DB 948 AAWAATATATATATATATATATATATATATATATATATATATATATATATAT 889
QY 771 GGGATGTAAGTGTCCCTGAATATATATATATATATATATATATATATATATAT 830
DB 888 WWAATWTATATATATATATATATATATATATATATATATATATATATATATAT 833
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QY 891 TTTAATTTAGTAGTACGTAAGTTTACATCATATAGGAGTATCTGTTGAGCAATCATCACT 950
DB 772 TAWAATATATATATATATATATATATATATATATATATATATATATATATATAT 713
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QY 1068 CCTTTTGGCGGTATCCACTACTGTTAATGAAGCTTTTAAATCACTGTTTGGGAG 1127
DB 592 TAWATTAATATATATATATATATATATATATATATATATATATATATATATAT 533
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DB 532 WAWTWAATAATATATATATATATATATATATATATATATATATATATATATAT 477

RESULT 10
BX335216

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LOCUS BX335216 1201 bp mRNA linear EST 02-MAY-2003
DEFINITION BX335216 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
clone CSODI012YG10 5-PRIME, mRNA sequence.
ACCESSION BX335216
VERSION BX335216.1 GI:30341402
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 714.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODI012BD05QP1&cluster=714.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODI012BD05QP1.
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sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
Query Match 5.5%; Score 66.8; DB 13; Length 1201;
Best Local Similarity 38.8%; Pred. No. 0.0016;
Matches 217; Conservative 46; Mismatches 295; Indels 2; Gaps 1;
QY 629 ATACGAAGAGAAATTTTGAATAATGAAGTGCATTTGCGGATTTTGATTCAGAAATAGCTT 688
DB 539 AAAAAAAMCHNNNNNNNNNNKGGVVCMMWMMGGTKGGGGTTTTTTTTWTWTWT 598
QY 689 TAATCTCAATTAACGTTTAAAGAGAGTGGTGATGAAGAGAGAGCCGATTTTCTTTG 748
DB 599 TWTTTTWWTAAANNNAANNAANNAANNAANNAANNAANNAANNAANNAANNAAN 658
QY 749 GACATGATATAGAGCAGGAAGGAGTAAAGTGTTCCTCGAATATATATATAGTACAAA 808
DB 659 AATATAAAAAAANAANAANAANAANAANAANAANAANAANAANAANAANAANA 718
QY 809 AGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAATGATTTTTTTTAAATAGTTATA 868
DB 719 ATTTTAATATTTTTTATTTTATTTTATTTTATATATATATATATATATATATAT 776
QY 869 AACTTTTITAGACTATCTTCATTTAATTCATAGTAGTAAAGTTTACATCATTTAGAGT 928
DB 777 AATTTTTTATAAATTTTWTATAAATTAATTTTTTTTTTTTTTTTTTTTTTTTATAT 836
QY 929 ATCTGTGTGAGCAATCATCACTTCGTTTACTGTGATCGTCACTACCATGATGAATTTT 988
DB 837 WTTTATTTTATAAATTTTWTTTTTTTTTTTTTTTTTTTTTTTTATNAAATTAATTAATA 896
QY 989 TTTTATAAGTCCCATCTCGAAAGTAATCCACATATACACAGTCTTATTAATCTCATCTTC 1048
DB 897 TATATATATATTTTTTNAATATATATATATATATATATATATATATATATATAT 956
QY 1049 TTCACTAATGTTAATTTTCCCTTTTGGCGGTATCCACTACTGTTAATGAATGTTTAA 1108

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Matches	129;	Conservative	59;	Mismatches	163;	Indels	0;	Gaps	0;
Qy	844	AAATGATTTTTTTTAAATGAAGTTATAAACCTTTTTTAGAACTATCTTCATTTAAATGATAGT	903						
Db	803	AHHHHHHHHWWAAAAAABAAWWWWTTWTANNNNNNNATTTTTTTTAAAAAAA	744						
Qy	904	ACGTAAGGTTTACATCATGAGAGTATCTGTGAGCAATCATCACCTTCGTTACTGTGAT	963						
Db	743	AAAWTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTATWAMAMMTATWAMTTTTT	684						
Qy	964	GGTCAACTACCCATATGAAATATTTTTTATAAGTCCCATCTCGAAGAGTAATCCACATAT	1023						
Db	683	WCTMCAYAWATATWTWATWHHTATWAAAAAAYATHATAWAAAAATATWTAWAAAAW	624						
Qy	1024	CACAGTCTATTAAATCTGATCCTCTTCATCATGTATGTTAAATTTCCTTTTTTCGGGTAT	1083						
Db	623	AAAAAAAAACATWTCAAAAATTTTTTTTTTTTTTTTATATATATTTTTTTTTTWTATAT	564						
Qy	1084	CCATCTGTTAATGAAGTGTTTTTTAATTCATCTGTTTTTGTGAGAAAGATATCCTTTTTG	1143						
Db	563	MTATAAWATATATATTTTTTTTTTTTTTTTTTTTTTTTATATATANMMMMHWAATWTWT	504						
Qy	1144	TTTTAAATGATCGACATGATATCTCTTTATTTCTGTGTTTCCTTAAAAAGA	1194						
Db	503	TTTWAATTTWTATAAAAATTTTTTTTTTTTWWAAATTTTTTTTTTTTAAATATATAT	453						

RESULT 13					
BX395112/c					
LOCUS	BX395112	1201 bp	mrna	linear	EST 13-MAY-2003
DEFINITION	BX395112 Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED Homo sapiens cDNA clone CS0DC029P03 5'-PRIME, mRNA sequence.				

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ACCESSION      BX395112
VERSION        GI:30628432
KEYWORDS
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
               1. (bases 1 to 1201)
               Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
               Full-length cDNA libraries and normalization
               Unpublished (2001)
               Contact: Genoscope
               Genoscope - Centre National de Sequencage
               BP 191 91006 EVRY cedex - France
               Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
               Library was constructed by Life Technologies, a division of
               Invitrogen. This sequence belongs to sequence cluster 10493.f For
               more information about this cluster, see
               http://www.genoscope.cns.fr/
               cgi-bin/cluster.cgi?seq=CS0DC029CH02QPI&cluster=10493.f. Contact :
               Feng Liang Email : fliang@lifetech.com URL :
               http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
               Faraday Avenue Genoscope sequence ID : CS0DC029CH02QPI.

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FEATURES
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1. 1201
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/db_xref="taxon:9606"
/clone="CS0DC029YP03"
/tissue_type="NEUROBLASTOMA COT 25-NORMALIZED"
/clone_lib="Homo sapiens NEUROBLASTOMA COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(GT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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Query Match	5.4%	Score	66.2	DB 13	Length	1201	
Best Local Similarity	35.8%	Pred. No.	0.0021				
Matches	225	Conservative	79	Mismatches	322	Indels	2
						Gaps	1

QY	560	ATTGAGACGAAAAATCCGGTCTGTATTATAAAGATTGATCGATACGATACGAAAGAG	639
Db	1168	RKWTDTAAAAAANKTKTKTKTKTWTTATWTTWTTTTTKTKTKTKTAWAAAAAAA	1109
QY	640	AATTTTGAAATGAAGTCGCATTTGCCGGATTTCATTACAGNAITTAGCTTTATCTTCATTT	699
Db	1108	AAAAAAAATWWAWAGTKTTTTTRWDWTATWTAWTATATAAKWGVTGTTKTGGGTRKAGG	1049
QY	700	AAACGTTTTAAAAGAAGTGGTGATGAAAGAGGAAGCGCATGTTTCTTTGGACATCATATA	759
Db	1048	ARWAADKTGRDRTGTGTRAGTGTGKTRAASAAAAATATAAAAAAAWATWTTTGWTTTR	989
QY	760	GAGCAGAAAGCGGATGTAAGTGTCCCTGAATATATAGTACAAAAAGTCATGAGCT	819
Db	988	AGAGTGTGTRXRTAKRAAGAKGTTKTTTKTTKWTTWTATATAAAAAARAARWGWDAA	929
QY	820	TATTGCGTCACTACTTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTTTTAG	879
Db	928	TATRTKTTKTAWGAAAAAANAANAANWNTTTATWTTAWAAWAAATTTATAWAA	869
QY	880	AACATCTCTCATTTAAATTGATAGTACGTGAAGTTTACATCATTAGGAGTATCTGTGTGAG	939
Db	868	AAAAAWATATATTTTTTTTTTTTTTTTTTTTWWAAKATTTTTTTTTTDRAAWATTTWAAAAA	809
QY	940	CAATCATCACTCTGTTACTGTGATGGTCAACTCCCATATGAATATTTTTTTTTATAGTCCC	999
Db	808	AAA--WATAWAAAAAAWWAWTTTGTTTWAAGADWTTTAAAGAAWWTATTTAAANWTT	751
QY	1000	CATCCTCGAAAGTAATCCAATATCAATCAAGTCTATAAATCTGATCCTCTTCATCTAATG	1059
Db	750	TT	691
QY	1060	TTAATTTTCCTTTTTTGGCGGTATCCCATCTGTTTAAGATGTTTTTAATCATCTGTTTT	1119
Db	690	TTTTTTTTTKTGTGTTNDT	631
QY	1120	TTGTGAAAAGATATCCTTTTTTTTGTTTTAATTTGACTCGACATGATATCTTTTATTTCTT	1179
Db	630	TTTTTTTTTTTTKKKKTT	571
QY	1180	GTTTTCCTAAAAAGACAGGGGGCTCATTT	1207
Db	570	TTTTTACCCTGAACACACCGTGGCTTATTT	543

RESULT 14
EX425658/c
LOCUS BX425658 981 bp mRNA linear EST 15-MAY-2003
DEFINITION BX425658 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
CLOB024ZH07 3-PRIME, mRNA sequence.

ACCESSION	BX425658
VERSION	BX425658.1
KEYWORDS	GI:30786491
SOURCE	EST.
ORGANISM	Homo sapiens (human)
REFERENCE	Homo sapiens
AUTHORS	Eukaryotica; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE	1 (bases 1 to 981)
JOURNAL	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
COMMENT	Full-length cDNA libraries and normalization Unpublished (2001) Contact: Genoscope

Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOCBB0242H07Pp1.

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FEATURES
source
    Location/Qualifiers
    1..981
    /organism="Homo sapiens"
    /mol_type="mRNA"
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FEATURES

ORIGIN

Search completed: February 24, 2004, 04:22:28
Job time : 2470 secs

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BX436510	Homo sapiens THYMUS Homo sapiens cDNA clone CSOCAP002YK09		
DEFINITION	5'-PRIME, mRNA sequence.		
ACCESSION	BX436510		
VERSION	BX436510.1 GI:30770190		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1200) Li,W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cdna libraries and normalization Unpublished (2001)		
AUTHORS	Contact: Genoscope		
JOURNAL	Genoscope - Centre National de Sequencage		
COMMENT	BP 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5393.f For more information about this cluster, see http://www.genospace.cns.fr/ cgi-bin/ccluster.cgi?seq=CSOCAP002AF05QP1&clicluster=5393.f . Contact :		

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 03:41:17 ; Search time 1437 Seconds
(without alignments)
2977.738 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgtttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2308684 seqs, 1750822206 residues

Total number of hits satisfying chosen parameters: 4617368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
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- 18: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59.8	4.9	3673778	14	US-10-312-841-2
2	57.8	4.7	673	12	Sequence 2, Appli
3	56	4.6	3673778	14	Sequence 57885, A
4	55.6	4.5	6419	14	Sequence 1, Appli
5	55.6	4.5	14006	14	Sequence 240, App
6	54.8	4.5	516	9	Sequence 1931, Ap
7	54.8	4.5	6109	12	Sequence 5785, Ap
8	54.8	4.5	6109	14	Sequence 33, Appl
9	53.4	4.4	6035	14	Sequence 299, App
10	53.4	4.4	15548	14	Sequence 1497, Ap
11	53.2	4.4	15732	14	Sequence 2128, Ap
12	53.2	4.4	15732	14	Sequence 95, Appl
13	53	4.3	6436	14	Sequence 107, App
14	53	4.3	8776	16	Sequence 654, App
15	52.8	4.3	158001	16	Sequence 150, App
GENERAL INFORMATION					

16	52.6	4.3	9539	14	US-10-239-676-52	Sequence 52, Appl
17	52.6	4.3	9539	14	US-10-240-453-54	Sequence 54, Appl
18	52.6	4.3	11178	12	US-10-221-613-16	Sequence 16, Appl
19	52.4	4.3	446	9	US-09-960-352-3400	Sequence 3400, Ap
20	52.4	4.3	5032	12	US-10-221-613-39	Sequence 39, Appl
21	52.2	4.3	6713	14	US-10-311-455-1053	Sequence 1053, Ap
22	52.2	4.3	6713	14	US-10-240-485-79	Sequence 79, Appl
23	52.2	4.3	10286	14	US-10-239-676-14	Sequence 14, Appl
24	52.2	4.3	10286	14	US-10-240-453-22	Sequence 22, Appl
25	52	4.3	17934	14	US-10-311-455-1692	Sequence 1692, Ap
26	51.8	4.2	5518	14	US-10-311-455-1304	Sequence 1304, Ap
27	51.6	4.2	7597	14	US-10-311-455-986	Sequence 986, App
28	51.4	4.2	5750	14	US-10-311-455-1981	Sequence 1981, Ap
29	51.4	4.2	9539	14	US-10-239-676-51	Sequence 51, Appl
30	51.4	4.2	9539	14	US-10-240-453-53	Sequence 53, Appl
31	51.2	4.2	5127	14	US-10-239-676-132	Sequence 132, App
32	51.2	4.2	6145	14	US-10-311-455-945	Sequence 945, App
33	51.2	4.2	14649	14	US-10-239-676-121	Sequence 121, App
34	51.2	4.2	14649	14	US-10-240-453-141	Sequence 141, App
35	51	4.2	17703	16	US-10-257-166-34	Sequence 34, Appl
36	50.8	4.2	5666	14	US-10-311-455-1746	Sequence 1746, Ap
37	50.8	4.2	7921	14	US-10-311-455-1944	Sequence 1944, Ap
38	50.8	4.2	15674	14	US-10-311-455-336	Sequence 336, App
39	50.8	4.2	15674	14	US-10-240-485-30	Sequence 30, Appl
40	50.6	4.1	6314	14	US-10-240-452-14	Sequence 14, Appl
41	50.4	4.1	5244	16	US-10-257-166-95	Sequence 95, Appl
42	50.4	4.1	7990	14	US-10-311-455-131	Sequence 131, App
43	50.4	4.1	7990	14	US-10-240-452-7	Sequence 7, Appli
44	50.2	4.1	6161	14	US-10-311-455-384	Sequence 384, App
45	50.2	4.1	6494	14	US-10-311-455-1366	Sequence 1366, Ap

ALIGNMENTS

RESULT 1

US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1

; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG

; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO

; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2

; SEQ ID NO 2

; LENGTH: 3673778

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

; NAME/KEY: unsure

; LOCATION: (379615)

US-10-312-841-2

Query Match 4.9%; Score 59.8; DB 14; Length 3673778;

Best Local Similarity 46.3%; Pred. No. 0.24;

Matches 196; Conservative 0; Mismatches 227; Indels 0; Gaps 0;

Qy	797	TATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAAGATTTTTTT	856
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Qy	857	AAATAGTTATAACTTTTTTGAACATCTCTTATTAAATGATAGTACCTAGGTTTAC	916
Db	1064898	AAATATTATTATTATTTTATATTTTTATGAAAATAATAGTATATGATTAGTTT	1064957

Qy	917	ATCATTAGGAGTATCTTGTGAGCAATCATCACTTCCTTACTGTGATGGTCAATCCCA	976
Db	1064958	TATGTAATTTGTTTGTGTTTATAGATTTTTAGAAAGTTCTTTTATGATATTATTAAGA	1065017

QY	977	TATGAATAATTTTTTATAAGTCCCATCTCCGAAAGTAATCCACATATCACAGTCTATTAA	1036
Db	1065018	AATAAGCTTTTAGAATTTAGGATGTATATTTAAATCGTAATTAATATATATATATTTGTATTTA	1065077
QY	1037	ATCTGATCCCTCTTCATCTAAATGTTAAATTTTCCTTTTTTTGGCGGTATCCATACTGTTAAAT	1096
Db	1065078	TATAAATTTGTTATATTTGTTAATTTTGAATTTTGAATTTTGTAGTTGAGTAAATATTTTGT	1065137
QY	1097	GAATGTTTTTAAATTCATCTGTTTTTGAGAAAGATATCCCTTTTTTGTATTTTAAATTTGACTC	1156
Db	1065138	TATTTTTTTTTTATTTGATTTGATTTTAAATTTATTTTATAATATATATATTTTGTTTTTAAAG	1065197
QY	1157	GACATGTATATCTTTTATTTCTTGTTTTCTTAAAGACAGGGGGCTCATTTGGGTCTCT	1216
Db	1065198	TTTGTATGATATAGTTTATTTATTTTTTTTATTAATGATTTATTTAAATTTTGT	1065257
QY	1217	TTG 1219	
Db	1065258	TTG 1065260	

RESULT 2

US-10-424-599-57885

; Sequence 57885, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J

; APPLICANT: Kovalic David K

; APPLICANT: Zhou Yihua

; APPLICANT: Cao Yongwei

; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated W

; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

; FILE REFERENCE: 38-21(53223)B

; CURRENT APPLICATION NUMBER: US/10/424,599

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 285684

; SEQ ID NO 57885

; LENGTH: 673

; TYPE: DNA

; ORGANISM: Glycine max

; FEATURE:

; NAME/KEY: unsure

; LOCATION: (1)..(673)

; OTHER INFORMATION: unsure at all n locations

; FEATURE:

; OTHER INFORMATION: Clone ID: PAT_MRT3847_23282C.1

; US-10-424-599-57885

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Db      604 TTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTCGTAATTTTATTATTTTTTTTTTTTTT 663
Qy      1179 TGTGTTT 1184
Db      664 TTTTTT 669

RESULT 3
US-10-312-841-1
; Sequence 1, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb d
; FILE REFERENCE: EOI/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 1
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (3294164)
US-10-312-841-1

Query Match 4.6%; Score 56; DB 14; Length 3673778;
Best Local Similarity 44.8%; Pred. No. 1.6;
Matches 215; Conservative 0; Mismatches 265; Indels 0; Gaps 0;

Qy      663 TCGGGGNTTGATTCAGAAATAGCTTTATCTTCAATTAAACGTTTAAAAGAAGCTGGTGAT 722
Db      2552436 TGGGATAATTTTTTTTTTAATTTATTATTGTTAAAGTTCTGTAAATGTTTAAAGAGTT 2552495
Qy      723 GAAAGAGAACGCCGATGTTTTCTTTGGACATGATATAGACAGGAAGGGGATGTAAAGT 782
Db      2552496 TTAATATAATTTTGTTATTAGATTTTGTGAGTTATTAGTTTAGAGCTTTTTCGTTT 2552555
Qy      783 GTTCCCTGGAATATATATAGTACAAAAAGCATGAGCTTATTCGCTCATGCATTTTCGTT 842
Db      2552556 GGTAATATAATAGAAATATTGTAATGGTTCGTAAATTTTGAGTTATATTGGTTGTTGTA 2552615
Qy      843 TAAATGATTTTTTTAAATAAGTTATAAACTTTTTTTTAGAACTATCTTCATTTAATTCATAG 902
Db      2552616 TTAGTTGTTTGTGTTTACGTCGGTTTAAATTTTTTTTTTTTAAATTAATAAATG 2552675
Qy      903 TAGTAAGGTTTACATCATTAGGAGTATCTGTTGAGCAATCATCATCTCGTTACTGTGA 962
Db      2552676 TTAGAATGGGTTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTTTTTTTTTTATTTTTTTT 2552735
Qy      963 TGGTCAACTACCACATATGAATATTTTTTTTATAAGTCCCATCCGAAAGTAATCCACATA 1022
Db      2552736 TTTTTTTTGTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2552795
Qy      1023 TCACAGTCTATTAATCTGATCCCTCTCATCTAAATGTTAAATTTTCCTTTTTTGGCGGTA 1082
Db      2552796 TTTTTTTTTTTTTTTTAAATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 2552855
Qy      1083 TCCATCTGTTAATGAATGTTTTTAATTCATCTGTTTTTGTGAGAAAGATATCCTTTTTT 1142
Db      2552856 TGTTTTAGTTTTTTTTTTTATTAGTTTGTATTTTATGTTGGTTTATTTTTTTTTT 2552915

RESULT 4
US-10-311-455-240
; Sequence 240, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander

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Query Match 4.5%; Score 54.8; DB 9; Length 516;
Best Local Similarity 46.0%; Pred. No. 0.038;
Matches 182; Conservative 0; Mismatches 214; Indels 0; Gaps 0;

QY 793 TATATAGTACAAAAGTCATGAGCTTATTCGCTCATGACTTTTCGTTTAAATGATTT 852
DB 38 TGTATAGAGTTTAAATCTTAAATGCAATAGGATATNGAGGTTAGTTTATATTTT 97

QY 853 TTTTAAATAGTTTAAACTTTTTTGAAGTATCTTCAATTAATGATAGTACGTAAAGT 912
DB 98 GTTTTGTATTAATTTTATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 157

QY 913 TTATCAATTTAGAGATCTTTGTGAGCAATCATCTTCGTACCTGATGTCACACTA 972
DB 158 TTATATTAAATTT 217

QY 973 CCCATATGAATATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACAGTCTA 1032
DB 218 TTTTATTTTTTTTTTTTATTTTATTTATTTTTTTTTTTTTTTTTTTTTTTA 277

QY 1033 TTAATCTGATCCTTCTTCACTAAAGTTAAATTTCCCTTTTGGCGGTATCCATCTGT 1092
DB 278 TATTTTATTTA 337

QY 1093 TAATGATGTTTAAATCTCTTTTCTGTTTCTGAGAAAGATATCCTTTTGTATTAATG 1152
DB 338 TAAATTTTGTATTTATTTTATTTTTTTTTTTTTTTTTTTTATTTTATTTTATTTT 397

QY 1153 ACTCGACATGATATCTTTTATTTCTTGTGTTTCCCTA 1188
DB 398 TTTTATTTTTTATTTTTTTTTTTTTTTTTTTTTTTA 433

RESULT 7
US-10-221-613-33
; Sequence 33, Application US/10221613
; Publication No. US20040029123A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle
; FILE REFERENCE: 5013.1004
; CURRENT APPLICATION NUMBER: US/10/221.613
; PRIOR FILING DATE: 2002-09-13
; PRIOR APPLICATION NUMBER: PCT/EP01/02945
; DE 10013847.00
; DE 10019058.8
; DE 10019173.8
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-03-15
; 2000-03-15
; 2000-04-06
; 2000-04-07
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 428
; SEQ ID NO 33
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (214, 2796..2797, 4347)
US-10-221-613-33

Query Match 4.5%; Score 54.8; DB 12; Length 6109;
Best Local Similarity 47.2%; Pred. No. 0.13;
Matches 167; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 835 TTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTTTGAAGTATCTTCAATTA 894
DB 1741 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1800

QY 895 ATTGATAGTACGTAAGGTTTACATCATTAAGGAGTATCTTGTGAGCAATCATCATTCT 954
DB 1801 TTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1860

QY 955 TACTGTGATGGTCAACTACCCATATGAATATTTTTTATAAGTCCCATCTCGAAAGTAA 1014
DB 1861 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1920

QY 1015 TCCACATATCACAGTCTTATAAATCTGATCCTTCTTCAATCAATTAATTTTCCCTTT 1074
DB 1921 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1980

QY 1075 TGCGGTATCCATPACTGTTAAATGAATGTTTTTAAATCAATCTGTTTTTGTGAGAAAGTAT 1134
DB 1981 CGTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2040

QY 1135 CCTTTTTTGTGTTTAAATGACTCGACATGATATCTTTTATTTCTTGTGTTTCCCTA 1188
DB 2041 TATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 2094

RESULT 8
US-10-311-455-299
; Sequence 299, Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311.455
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: PCT/EP01/07537
; PRIOR FILING DATE: 2001-07-02
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 2424
; SEQ ID NO 299
; LENGTH: 6109
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: 214, 2796..2797, 4347
; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-299

Query Match 4.5%; Score 54.8; DB 14; Length 6109;
Best Local Similarity 47.2%; Pred. No. 0.13; Indels 0; Gaps 0;
Matches 167; Conservative 0; Mismatches 187; Indels 0; Gaps 0;

QY 835 TTTTCGTTTAAATGATTTTTTAAATAAGTTATAAACTTTTTTGAAGTATCTTCAATTA 894
DB 1741 TTTTATTAATGATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1800

QY 895 ATTGATAGTACGTAAGGTTTACATCATTAAGGAGTATCTTGTGAGCAATCATCATTCT 954
DB 1801 TTTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1860

QY 955 TACTGTGATGGTCAACTACCCATATGAATATTTTTTATAAGTCCCATCTCGAAAGTAA 1014
DB 1861 TTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 1920

Query Match	Score	DB	Length	Mismatches	Indels	Gaps
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1
US-10-239-676-95						
796	4.4%	53.2	14	15732	1	1
Best Local Similarity	47.5%	0	0.45	0	0	0
Matches	189	Conservative	0	208	1	1


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Db 3000 TATTATTAATAAATATTTTATTTATTTTAAAGCGTTATTCGATTTTATAAATTATTA 3059
Qy 853 TTTTAAATAAGTTATAAATTTTTTTTAGAAGTATCTTCAATTTAAATGATAGTACGTAAGGT 912
Db 3060 TTTTAAATTTATTTATTAAGTTAGAAAAAATGATATATTTAATGATTTGTAAGAAATAT 3119
Qy 913 TTACATCATAGGAGTATCTTTGTTGAGCAATCATCTCTCTTACTGTGATGGTCAACTA 972
Db 3120 TTTAATTTAGGGTTATGAAGAAAGGTATTTTGAATTAATGAATATAGTGGAAATA 3179
Qy 973 CCCATATGAATAATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACAGTCTA 1032
Db 3180 TAAATATATATGATAAAATTTTTGATAGTTGAGGATATGAATGAAAAATTAATTTT 3239
Qy 1033 TTAATCTGATCTCTCTCTCACTCAATGTTAAATTTTCCCTTTTTTGGCGGTATCCACTGTT 1092
Db 3240 TTTGTTTTTTTTTTTTTTAGTTGTTATTTGATTAATTAAGTTTTTTTTTTTTTTTTTTT 3299
Qy 1093 TAAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCTCTTTTGTGTTTAAATG 1152
Db 3300 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3359
Qy 1153 ACTCGACATGATATCTTTTATTTCTTCTGTTTCTCTAA 1189
Db 3360 TTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTT 3396

RESULT 14
US-10-257-166-150
; Sequence 150, Application US/10257166
; Publication No. US20040023230A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
; TITLE OF INVENTION: Genes Implicated in Pharmacogenomics
; FILE REFERENCE: 5013.1011
; CURRENT APPLICATION NUMBER: US/10/257.166
; CURRENT FILING DATE: 2002-10-07
; PRIOR APPLICATION NUMBER: PCT/EP01/07470
; DE 10032529.7
; DE 10043826.1
; PRIOR FILING DATE: 2001-06-29
; 2000-06-30
; 2000-09-01
; NUMBER OF SEQ ID NOS: 178
; SEQ ID NO 150
; LENGTH: 8776
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-150

Query Match 4.3%; Score 53; DB 16; Length 8776;
Best Local Similarity 46.8%; Pred. No. 0.37;
Matches 167; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

Qy 832 ACTTTTCGTTTAAATGATTTTAAATAGTTTATAAAGTTATAAAGTCTTTTGAAGTATCTTCAT 891
Db 6852 AATATATTGGAAATTAATTTTAAATATATTTTAAATATATTTTAAATATATTTTGAATTTTGA 6911
Qy 892 TTAATGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGTGAGCAATCATCACTT 951
Db 6912 ATATTTTTTGTGTTTGGTATAAAATGTAATTTAGGTTTATTTTGAATATTTTAAATTT 6971
Qy 952 CGTTACTGTGATGTCACACTACCCATATGAATATTTTATAAGTCCATCCCTCGAAG 1011
Db 6972 TGGTTTTGGAATAGTTATTTTAAAAAGTTTTTGGTTTTTTTTTAGTGGAAAAATGGTAT 7031
Qy 1012 TAAATCCACATATCAGTCTATTAATCTGATCTCTCTCATCTAATGTTAATTTTCTT 1071
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Db 7032 TAATAAGTTAAGATTTGGTTATTAAGTGTGTTTATTTGTTATTTGAAAATGTTATTTGTTATTT 7091
Qy 1072 TTTTGGCGGTATCCATATCTGTTTAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGA 1131
Db 7092 AGTTTATTAGTGGAGAGAGTACGGAGTATATGTTTTTTTGTATATATATAATAATATA 7151
Qy 1132 TATCCTTTTTTTGTTTTTAAATGACGTCGACATGATATCTTTTATTTCTTTGTTTCTTA 1188
Db 7152 TATATATATTATGTTTATTTAAATTAATTTTGGTTTTTTTTTGTATTTTATTTATTTA 7208

RESULT 15
US-10-211-179-11/c
; GENERAL INFORMATION:
; APPLICANT: Nicholas M. Dean
; APPLICANT: Kenneth W. Dobie
; TITLE OF INVENTION: ANTIGENSE MODULATION OF PHOSPHOTYROSYL PHOSPHATASE ACTIVATOR EXPRI
; FILE REFERENCE: PUS-0011
; CURRENT APPLICATION NUMBER: US/10/211.179
; CURRENT FILING DATE: 2002-08-01
; NUMBER OF SEQ ID NOS: 119
; OTHER INFORMATION: n = a, t, c, or g
US-10-211-179-11

Query Match 4.3%; Score 52.8; DB 16; Length 158001;
Best Local Similarity 43.2%; Pred. No. 1.7;
Matches 252; Conservative 0; Mismatches 332; Indels 0; Gaps 0;

Qy 608 TATTAACGATTGATCGTATACGAAAGAGAAATTTTGAAAAAGAGTGCATTTCCGG 667
Db 127542 TATTATATATATATATTTTATATATATATATATATATATATATATATATATATATATATAT 127483
Qy 668 GATTGATTGAGAAATAGCTTTATCTTCAATTAACGTTTTAAAAAGAGTGTGATGAAG 727
Db 127482 TATTTTTTATATATATATATATTTTATATATATATATATATATATATATATATATATATAT 127423
Qy 728 AGAAGCCGATGTTTCTTTGGACATGATATAGACGAGGAAGGGATGTAAGTGTTCC 787
Db 127422 ATATTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 127363
Qy 788 CTGAATATATATAGTACAAAAAGTCATGAGCTTATTCGCTCATGACATTTTTCGTTTAAAT 847
Db 127362 TTTTATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 127303
Qy 848 GATTTTTTAAATAAGTTATAAACTTTTTTAGAACTATCTTCAATTTAATTCATAGTAGCT 907
Db 127302 TATATATTTTATATATATATATATATATATATATATATATATATATATATATATATATAT 127243
Qy 908 AAGTTTACATCATTAGGAGTATCTTTGAGCAATCATCACITTCGTTACTGTGATGGTC 967
Db 127242 ATATATTTATATATTTTATATATATATATATATATATATATATATATATATATATATAT 127183
Qy 968 AACTTACCATATGAATATTTTTTATAAGTCCCATCTCGAAAGTAATCCACATATCACA 1027
Db 127182 TATAATATATATATATATATTTTATATATATATATATATATATATATATATATATATAT 127123
Qy 1028 GTCATTAAATCTGATCCCTTTCATCTAATGTTAAATTTTCCCTTTTTTGGCGGTATCCAT 1087
Db 127122 TATTTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 127063
Qy 1088 ACTGTTAAATGAATGTTTTTAAATTCATCTGTTTTTGTGAGAAAGATATCCCTTTTGTGTTT 1147
Db 127062 TATTATATATATACAAATTAATAATATATATATATATATATATATATATATATATATATAT 127003
Qy 1148 AATTTGCTCGACATGATATCTTTTATTTCTGTTTCTCTAAAA 1191
Db 127002 TTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 126959

Search completed: February 24, 2004, 05:42:50
Job time : 1456 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:02:27 ; Search time 415 Seconds
(without alignments)
12509.152 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 cttactgtattgtttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq_29Jan04.*

- 1: geneseqn1980s.*
- 2: geneseqn1990s.*
- 3: geneseqn2000s.*
- 4: geneseqn2001as.*
- 5: geneseqn2001bs.*
- 6: geneseqn2002s.*
- 7: geneseqn2003as.*
- 8: geneseqn2003bs.*
- 9: geneseqn2003cs.*
- 10: geneseqn2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1222	100.0	1222	5	Aaf29642 Listeria
2	1037	84.9	1339	6	Abk47468 DNA encod
3	644.2	52.7	753	6	Abk47472 DNA encod
4	633.6	51.8	753	6	Abk47471 DNA encod
5	623.4	51.0	753	6	Abk47470 DNA encod
6	620.2	50.8	753	6	Abk47469 DNA encod
7	617	50.5	753	6	Abk47474 DNA encod
8	617	50.5	753	6	Abk47473 DNA encod
9	615.4	50.4	753	6	Abk47475 DNA encod
10	613.8	50.2	753	6	Abk47476 DNA encod
11	57	4.7	8056	7	Abz10246 Haematopo
12	56.6	4.6	7667	4	Aas46334 Tumour su
13	55.6	4.5	6419	6	Abi32267 Human imm
14	55.6	4.5	14006	6	Abi33958 Human imm
15	55.6	4.5	47108	6	Abk31511 Signal tr
16	54.8	4.5	516	7	Abx40620 Bovine ES
17	54.8	4.5	6109	6	Abi32326 Human imm
18	54.8	4.5	6109	6	Aas61077 Human gen
19	54.6	4.5	9742	6	Abi70479 Chemicall
20	54.6	4.5	11964	6	Abq67025 Human ang
21	54	4.4	975	6	Abq29508 Oligonuc
22	54	4.4	975	6	Abq29509 Oligonuc
23	53.8	4.4	61020	4	Aas46788 Tumour su

24	53.4	4.4	6035	6	ABL33524	Human imm
25	53.4	4.4	8056	7	ABZ10100	Haematopo
26	53.4	4.4	15548	6	ABL34155	Human imm
27	53.2	4.4	594	6	ABQ46990	Oligonuc
28	53.2	4.4	594	6	ABQ46991	Oligonuc
29	53.2	4.4	8056	7	ABZ10246	Haematopo
30	53.2	4.4	15732	4	AAS45388	Chemicall
31	53.2	4.4	15732	6	ABK28233	DNA trans
32	53	4.3	6436	6	ABL32681	Human imm
33	53	4.3	8776	6	ABK40068	Human che
34	52.6	4.3	9539	4	AAS45347	Chemicall
35	52.6	4.3	9539	6	ABK28180	DNA trans
36	52.6	4.3	11178	6	ABK31173	Signal tr
37	52.6	4.3	11178	6	ABL70508	Chemicall
38	52.6	4.3	11178	6	AAS61060	Human gen
39	52.4	4.3	446	7	ABX38235	Bovine ES
40	52.4	4.3	5032	6	AAS61083	Human gen
41	52.4	4.3	8079	6	ABL92313	Chemicall
42	52.2	4.3	6713	6	ABL33080	Human imm
43	52.2	4.3	6713	6	ABL34526	Human met
44	52.2	4.3	6713	6	ABL70251	Chemicall
45	52.2	4.3	7143	3	AAA70250	Plasmodiu

ALIGNMENTS

RESULT 1

AAF29642	AAF29642 standard; DNA; 1222 BP.
XX	
AC	AAF29642;
XX	
DT	10-APR-2001 (first entry)
XX	
DE	Listeria sp. strain 240B1 aiiA gene.
XX	
KW	Listeria; aiiA; autoinducer inactivation protein A; antibacterial;
KW	disease resistance; soft rot disease resistance; bacterial infection; ds.
XX	
OS	Listeria sp.
XX	
PN	W0200102578-A1.
XX	
PD	11-JAN-2001.
XX	
PF	17-NOV-1999; 99WO-SG000128.
XX	
PR	02-JUL-1999; 99SG-00003146.
XX	
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY 1 RES LINK.
XX	
PI	Lian-Hui Z, Yihu D, Jinling X;
XX	
DR	WPI; 2001-138146/14.
XX	
DR	P-PSDB; AAS0476.
XX	
PT	New bacterial autoinducer inactivation proteins and nucleic acids
PT	encoding the protein, for increasing disease resistance, preventing or
PT	reducing bacterial damage to a plant or animal, or treating bacterial
PT	infections in animals.
XX	
PS	Claim 2; Fig 4A; 49pp; English.
XX	

The present sequence is a nucleic acid encoding a bacterial autoinducer inactivation protein (AiiA). It is useful for increasing disease resistance as well as preventing or reducing bacterial damage to a plant or animal. The nucleic acid may be used to confer resistance to diseases where expression of pathogenic genes are regulated by autoinducers, such as diseases caused by *Pseudomonas aeruginosa*, *Erwinia stewartii*, *Xenorhabdus nematophilus*, *Erwinia chrysanthemi*, *Pseudomonas solanacearum* and *Xanthomonas campestris*. It may also be used to confer soft rot disease resistance in susceptible plants such as potato, eggplant,

CC Chinese cabbage, carrot and celery. The bacterial autoinducer
CC inactivation protein may be directly used to treat or prevent bacterial
CC infections in animals including humans
XX
SQ Sequence 1222 BP; 376 A; 180 C; 238 G; 428 T; 0 U; 0 Other;

Query Match 100.0%; Score 1222; DB 5; Length 1222;
Best Local Similarity 100.0%; Pred. No. 5,8e-251;
Matches 1222; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CTTTACTGTATCTTTTATTCAAACTAAAGTGAAGTGAATGATGACAGTAAAG 60
Db |||||||
QY 1 CTTTACTGTATCTTTTATTCAAACTAAAGTGAAGTGAATGATGACAGTAAAG 60
Db |||||||
QY 61 AAGCTTTTATTCGTCGCCAGCAGGTCGTTGATGTGTGGATCATTCGTCGTTAATGATGAC 120
Db |||||||
QY 61 AAGCTTTTATTCGTCGCCAGCAGGTCGTTGATGTGTGGATCATTCGTCGTTAATGATGAC 120
Db |||||||
QY 121 TTAACACCGAGAGATTAATGAGCTTACCGGTTTGGTGTATCTTTTGGAGACTGAAGAA 180
Db |||||||
QY 121 TTAACACCGAGAGATTAATGAGCTTACCGGTTTGGTGTATCTTTTGGAGACTGAAGAA 180
Db |||||||
QY 181 GGACCTATTATTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAATGAAGTCTTTT 240
Db |||||||
QY 181 GGACCTATTATTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAATGAAGTCTTTT 240
Db |||||||
QY 241 AACGGTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAGATAGATCGTG 300
Db |||||||
QY 241 AACGGTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAGATAGATCGTG 300
Db |||||||
QY 301 AATATTTTAAACCGGTTGTTATGAGCCGGAAGACCTCTTTATATTAATGATGTTCTCAC 360
Db |||||||
QY 301 AATATTTTAAACCGGTTGTTATGAGCCGGAAGACCTCTTTATATTAATGATGTTCTCAC 360
Db |||||||
QY 361 TTGCATTTTATGATATGACAGAGAAATGCGCTTTTATAATACCAATCATTTGATGAC 420
Db |||||||
QY 361 TTGCATTTTATGATATGACAGAGAAATGCGCTTTTATAATACCAATCATTTGATGAC 420
Db |||||||
QY 421 CGTGCTGAATATGAGCGGCGCAGCATAGCGAAGATATTTGAAGAAATGATATGTCGG 480
Db |||||||
QY 421 CGTGCTGAATATGAGCGGCGCAGCATAGCGAAGATATTTGAAGAAATGATATGTCGG 480
Db |||||||
QY 481 AATTTAACTACAAATCATTTGAGGTGATTAAGTCTGATGAGTCTGACAGAGTCAATATTG 540
Db |||||||
QY 481 AATTTAACTACAAATCATTTGAGGTGATTAAGTCTGATGAGTCTGACAGAGTCAATATTG 540
Db |||||||
QY 541 CATACACAGGCCATATCTCCAGGCGCATCAATCGCTATTAAATGAGACAGAAATCCGGT 600
Db |||||||
QY 541 CATACACAGGCCATATCTCCAGGCGCATCAATCGCTATTAAATGAGACAGAAATCCGGT 600
Db |||||||
QY 601 CCTGTATTATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db |||||||
QY 601 CCTGTATTATTAACGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 660
Db |||||||
QY 661 TTTGCGGGATTTGATTCAGANTTACGTTTATCTTCAATTAACGTTTAAAGAGAGTGGTG 720
Db |||||||
QY 661 TTTGCGGGATTTGATTCAGANTTACGTTTATCTTCAATTAACGTTTAAAGAGAGTGGTG 720
Db |||||||
QY 721 ATGAAAGAGAGCCGATTTGTTTCTTTGGACATGATATGAGCAGGAGGAGGATGATAA 780
Db |||||||
QY 721 ATGAAAGAGAGCCGATTTGTTTCTTTGGACATGATATGAGCAGGAGGAGGATGATAA 780
Db |||||||
QY 781 GTGTTCCCTGAT 840
Db |||||||
QY 781 GTGTTCCCTGAT 840
Db |||||||
QY 841 TTTAAATGATTTTTTAAATGATTTAATAAGTTATATAAATTTTAAAGTCTTCAATTAATGAT 900
Db |||||||
QY 841 TTTAAATGATTTTTTAAATGATTTAATAAGTTATATAAATTTTAAAGTCTTCAATTAATGAT 900
Db |||||||
QY 901 AGTACGTAGGTTTACATCATTTAGGAGTATCTTGTGTAGCAATCATCTCGTACTGT 960
Db |||||||
QY 901 AGTACGTAGGTTTACATCATTTAGGAGTATCTTGTGTAGCAATCATCTCGTACTGT 960
Db |||||||

QY 961 GATGTCACACTCCCATATGAAATATTTTATAAGTCCCATCTCGAAAGTAAATCCACA 1020
Db |||||||
QY 961 GATGTCACACTCCCATATGAAATATTTTATAAGTCCCATCTCGAAAGTAAATCCACA 1020
Db |||||||
QY 1021 TATCACAGTCTATTAATAATCTGATCCTTCTTCACTAATGTAATTTTCTTTTGGCGG 1080
Db |||||||
QY 1021 TATCACAGTCTATTAATAATCTGATCCTTCTTCACTAATGTAATTTTCTTTTGGCGG 1080
Db |||||||
QY 1081 TATCCATACGTTTAAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCCTTTT 1140
Db |||||||
QY 1081 TATCCATACGTTTAAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCCTTTT 1140
Db |||||||
QY 1141 TTGTTTTTAAATGACTCGACATGATATCTTTTATTTCTTTTCTTAAAGACAGCGG 1200
Db |||||||
QY 1141 TTGTTTTTAAATGACTCGACATGATATCTTTTATTTCTTTTCTTAAAGACAGCGG 1200
Db |||||||
QY 1201 GCTCAATTTGGTCTCTTTTGAGT 1222
Db |||||||
QY 1201 GCTCAATTTGGTCTCTTTTGAGT 1222
Db |||||||

RESULT 2
ABK47468
ID ABK47468 standard; DNA; 1339 BP.
XX
AC ABK47468;
XX
DT 29-AUG-2002 (revised)
DT 18-JUN-2002 (first entry)
XX
XX DNA encoding autoinducer inactivation protein AiiC.
DE
XX Autoinducer inactivation; AiiC; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX
OS Bacillus thuringiensis; Cot1.
XX
FH Key Location/Qualifiers
FT CDS 166..918
FT /*tag= a
FT /product= "AiiC"
FT /note= "Autoinducer inactivation protein"
XX
FN WO200216623-A1.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
XX Zhang L, Dong Y, Xu J, Zhang H;
XX
XX WPI; 2002-304123/34.
XX
XX P-PSDB; AAU78804.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
XX having polynucleotide, and protein useful for increasing resistance to a
XX disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX Claim 4; Fig 8; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
XX autoinducer (N-acyl-homoserine lactone) inactivation protein. The
XX polynucleotide is useful for increasing disease resistance in a plant or
XX animal by introducing a polynucleotide into a cell of such a plant or
XX animal, in a manner that allows the cell to express the gene. The protein
XX is useful for reducing bacterial damage to a plant or animal preferably
XX human; and for reducing the formation of bacterial biofilms, by exposing

CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiC, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 1339 BP; 425 A; 196 C; 251 G; 467 T; 0 U; 0 Other;

Query Match 84.9%; Score 1037; DB 6; Length 1339;
Best Local Similarity 90.6%; Pred. No. 1.6e-211;
Matches 1106; Conservative 0; Mismatches 115; Indels 0; Gaps 0;

QY 2 TTTACTGTATTGTTTATTCACAACTAAATGTAAGGTGGATACATATGACAGTAAAGA 61
DB TTTACTGTATTGTTTATTCACAACTAAATGTAAGGTGGATACATATGACAGTAAAGA 178

QY 62 AGCTTTATTCGTCGACGAGTGGTGTATGTTGGATCATCTGCTGTTAATAGTACAT 121
DB AGCTTTATTCGTTCCAGCAGCTGGTGTATGTTAGATCATCTCTGTTAATAGTACAA 238

QY 122 TAACACAGGAGAAATTATTAGACTTACCGGTTTGGTGTATCTTTTGGAGACTGAAGA 181
DB TCGGCGCGGAAATTTATTGAACTTACCTGTATGGTGTATCTTTTGGAGCGGAAGA 298

QY 182 GACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTTAATTAAGGCTCTTTTA 241
DB GTCCCATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTTAATTAAGAACTTGTTG 358

QY 242 ACGGTACATTTGTGCAAGGGCAGGTTTACGAAATGACGTGAAGAGATGATCGTGA 301
DB AAGGGACATTTGCAAGAGGACAGAAATTTACGAAATGACGTGAAGAGATGATGAATAG 418

QY 302 ATATTTTAAACGGGTTGGTTATCAGCGGAGACCTTTTATATATTAGTTCTCACT 361
DB CTATTTTAAACGGTGAGGGTATGAGCCAGATGACCTCTCTTATATTATTAGTTCACT 478

QY 362 TGCATTTTGTATGATGAGGAGAAATGCGCTTTTATAAATPACCAATCATTTGACAGC 421
DB TGCATTTTGTATGATGAGGAGAAATGCGCTTTTATAAATPACCAATCATTTGACAGC 538

QY 422 GTGCTGAATATGAGCGCGCAGCATAGCAGAAATATTGAAAGATGTATATTGCGGA 481
DB GTGCTGAATATGAGCGCGCAGCATATAGAGAGAAATATTGAAAGATGTATATTGCGGA 598

QY 482 ATTTAAACTACAAATCATTTGAAGGTGATTTAGAGTGTACAGGAGTTCAATTATTGC 541
DB ATTTGAAGTACAAATTTATTGAAGGGATTTAGAGTGTACAGGAGTTTCAACTATTGT 659

QY 542 ATACACAGGCCATPACTCCAGGGCATCAATCGCTATTAAATTGACAGAGAAAAATCCGGTC 601
DB ATACACAGGACATTTACAGGGCATCAGTCACATTAATTGACAGAGAAAAATCTGGTG 718

QY 602 CTGTATTATTAAAGATTTGATGATCGTATACGAAAGAAATTTGAAATGAAAGTGCAT 661
DB TTGTTGTTATTAAACCATTTGATGATCGTATACGAAAGAAATTTGAAAGATGAAGTACCGT 778

QY 662 TTGCGGATTTGATTCAGAAATGATCTTATCTTCAATTTAAACGTTTAAAGAGAGTGTGA 721
DB TTGCTGATTTGATTCAGAAATGATCTTATCTTCAATTTAAACGTTTAAAGAGAGTGTGA 836

QY 722 TGAAGAGAGCCGATTTGTTTCTTTGGACATGATATAGACGAGAAAGGGGATGTAAG 781
DB TGAAGAGAGCCGCTTGTGTTCTTTCTTTGGACATGATATAGACGAGAAAGGGGATGTAAG 898

QY 782 TGTTCCCTGAATATATATAGTACAAAAGCATGAGCTTATTCGCTCATGACTTTTTCGT 841
DB TGTTCCCGGAATATATATAGTACAAAAGCATGAGCTTATTCGCTCATGACTTTTTCGT 958

QY 842 TTAATGATTTTTTAAATAGTTATTAACCTTTTGTAGAACTATCTTCATTTAATTGATA 901

DB TTAATGATTTTTTAAATAGTTATTAACCTTTTGTAGAACTATCTTCATTTAATTGATA 1018
QY 902 GTACGTAAAGGTTTACATCATTTAGAGATATCTTGTGTGCAATCATCTTCTGTTACTGTG 961
DB GTACGTAAAGGTTTACATCATTTAGAGATATCTTGTGTGCAATCATCTTCTGTTACTATG 1078
QY 962 ATGCTCAACTACCATATGAAATATTTTATTAAGTCCCATCTCGAAAGTAATCCACAT 1021
DB ATGATCAACTACCATATGAAATATTTTATTAAGTCCCATCTCGAAATGTAATCCACAT 1138
QY 1022 ATCACAGTCTATTAAATCTGATCTCTTCTCATCTAATGTTAATTTCTCTTTTGGCGGT 1081
DB ATCAATCTATTAAATCTGATCTCTTCTCATCTAATGTTAATTTCTCTTTTGGCGGT 1198
QY 1082 ATCCATCTGTTAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCTCTTTT 1141
DB ATTCATCTGTTAATGAATGTTTAAATTCATCTGTTTGTGAGAAAGATATCTCTTTT 1258
QY 1142 TGTTTAAATGACTGACATGATATCTTTTATTTCTGTTTCTTAAAGAGACAGGGG 1201
DB TGTTTAAATGACTGACATGATATCTTTTATTTCTGTTTCTTAAAGAGACAGGGG 1318
QY 1202 CTCATTTGGGTCCTCTTTGAGT 1222
DB CTCATTTGGATCCCTTTGAGT 1339

RESULT 3
ABK47472
ID ABK47472 standard; DNA; 753 BP.
XX
AC ABK47472;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
DE DNA encoding autoinducer inactivation protein AiiG.
KW Autoinducer inactivation; AiiG; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*; gene; ds.
XX
OS *Bacillus thuringiensis*; B18.
XX
FH Key Location/Qualifiers
CDS 1..753
FT /*tag= a
FT /product= "AiiG"
FT /note= "Autoinducer inactivation protein"
XX
FN WO200216623-A1.
XX
XX 28-FEB-2002.
XX 23-AUG-2000; 2000WO-SG000123.
XX 23-AUG-2000; 2000WO-SG000123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
XX Zhang L, Dong Y, Xu J, Zhang H;
XX
XX WPI; 2002-304123/34.
XX P-PSDB; AAU78808.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
XX having polynucleotide, and protein useful for increasing resistance to a
XX disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX Claim 4; Fig 9; 82pp; English.
XX
CC The invention describes an isolated polynucleotide encoding an

CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human, and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This sequence encodes the autoinducer inactivation protein AiiF, the
 CC autoinducer inactivation activity of which is studied in the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 753 BP; 243 A; 108 C; 172 G; 230 T; 0 U; 0 Other;

Query Match 52.78; Score 644.2; DB 6; Length 753;
 Best Local Similarity 91.08; Pred. No. 7.8e-128;
 Matches 685; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTGGATCATTCGCT 108
 DB 1 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTGGATCATTCGCT 60
 QY 109 GTTAATAGTACATTAAACAGGAGAAATATTAGACTTACCGGTTTGGTGTATCTTTG 169
 DB 61 GTTAACAGTGGTTAAACCGGGGAAAACATTAAACTTTGCCGTTTGGTGTATCTTTG 120
 QY 169 GAGACTCAAGAGAGCACTTTTATAGTAGACAGGTATGCCAGAAAGTGCAGTTAATAAT 228
 DB 121 GAGACGGAAGAGGTCCTATTTTAGTAGACACAGGTATGCCAGAAAGTGCAGTTAATAAT 180
 QY 229 GAAGGCTCTTTTAAACGGTACATTTTTCGAGGGCAGGTTTTTACCGAAAATGACTGAAGAA 288
 DB 181 GAAGGCTCTTTTAAACGGTACATTTTGCAAAAGGACAGATTTTACCGAAAATGACTGAAGAA 240
 QY 289 GATAGAAATCGTAATTTTAAACGGGTTGGTTATGACCGCGGAGACCTCTTTATATT 348
 DB 241 GATAGAAATCGTAATTTTAAACGGGTTGGTTATGACCGCGGAGACCTCTCTATATT 300
 QY 349 ATTAGTTCTCACTTGCATTTTATGATCATGCAGAGGAAATGCGCTTTTATAAATACACCA 408
 DB 301 ATTAGTTGCGCACTTGCATTTTATGATCATGCAGAGGAAATGCGCTTTTGAATACGCCA 360
 QY 409 ATCATTTGTACAGCGTGTGTAATATGAGCGCGGAGCATATGCGGATTAATTTGAAAGAA 468
 DB 361 ATCATTTGTACAGCGTGTGTAATATGAGCGCGGAGCATATGCGGATTAATTTGAAAGAG 420
 QY 469 TGTATATGCGGAATTTAACTACAAATCAATTGAAGGTGATTATGAAGTCGTACCAGGA 528
 DB 421 TGCATATCCAGATTTTAACTACAAATTTATGAAGGTGATTATGAAGTCGTACCTGGT 480
 QY 529 GTTCAATTTATGATACACAGGCGCATCTCAGGGCATCAATCGCTATTAAATGAGACA 588
 DB 481 GTTCGGTTATGTAATACACAGGACATCTCCAGGCGATCACTCATTTAATTTGAGACG 540
 QY 589 GAAAAATCCGGTCTGTATTTAATTAACGATTCATCGATCGATATACGAAAGAGAAATTTGAA 648
 DB 541 GAAAAATCCGGTCTGTATTTAATTAACGATTCATCGATCGATATACGAAAGAGAAATTTGAA 600
 QY 649 AATGAAGTGCATTTGGGGATTTGATTCAGAAATAGCTTTATCTTCAATTAACGTTTA 708
 DB 601 GATGAAGTACCGTTTGGCGGATTTGATTCGGAATTTAGCCTTTATCTTCAATTAACGTTTA 660
 QY 709 AAAGAAGTGGTGTATGAAGAGAGAGCCGATTTGTTTCTTTGACATGATATAGACAGGAA 768
 DB 661 AAAGAAGTGGTGTATGAAGAGAGAGCCGATTTGTTTCTTTGACATGATATAGACAGGAA 720
 QY 769 AGGGATGTAAAGTGTTCCTCGAATATATAG 801
 DB 721 AAGGATGTAAAGTGTTCCTCGAATATATAG 753

RESULT 4

ABK47471
 ID ABK47471 standard; DNA; 753 BP.

XX ABK47471;

AC 29-AUG-2003 (revised)

DT 18-JUN-2002 (first entry)

XX DNA encoding autoinducer inactivation protein AiiF.

XX Autoinducer inactivation; AiiF; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; *Erwinia carotovora*; gene; ds.

XX *Bacillus thuringiensis*; B17.

XX Key Location/Qualifiers

PH 1..753

FT /*tag= a

FT /product= "AiiF"

FT /note= "Autoinducer inactivation protein"

XX WO200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG000123.

XX 23-AUG-2000; 2000WO-SG000123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J, Zhang H;

XX WPI: 2002-304123/34.

XX P-PSDB; AAU78807.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to a
 PT disease in sustainable plant or animal and for reducing bacterial damage.

XX Claim 4; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human, and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This sequence encodes the autoinducer inactivation protein AiiF, the
 CC autoinducer inactivation activity of which is studied in the invention.
 CC (Updated on 29-AUG-2003 to standardise OS field)

XX SQ Sequence 753 BP; 245 A; 105 C; 167 G; 236 T; 0 U; 0 Other;

Query Match 51.8%; Score 633.6; DB 6; Length 753;

Best Local Similarity 90.2%; Pred. No. 1.4e-125;

Matches 678; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTGGATCATTCGCT 108

DB 1 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGTCGTTGTATGTGGATCATTCCTCT 60

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QY 109 GTTAATAGTACATTAACACAGGAGAAATATTAGACTTACCGTTTGGTGTATCTTTTG 168
Db 61 GTTAATAGTACACTCGCCCGGGAAATTTATGAACCTTACCTGTATGTTGTATCTTTTG 120
QY 169 GAGACTGAAGAAGGACCTATTATTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT 228
Db 121 GAGACAGAAGAGGGCCCTATTATTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT 180
QY 229 GAAGTCTTTTAAACGGTACATTTTCGAAGCGCAGGTTTACCGAAAATGACTGAAGAA 288
Db 181 GAAGGCTTTTAAACGGTACATTTTCGAAGCGCAGATTTTACCGAAAATGACTGAAGAA 240
QY 289 GATAGAAATCGTAATTTTAAACGGCTTGTATGAGCGGAGACCTTCTTTATATT 348
Db 241 GATAGAAATCGTAATTTTAAACGGCTTGTATGAGCGGAGACCTTCTTTATATT 300
QY 349 ATTAGTCTCACTTTCATTTTATGATCGACGAGGAAATGGCGCTTTTATAAATACACCA 408
Db 301 ATTAGTCTCACTTTCATTTTATGATCGACGAGGAAACGGTCTTTTACAATACACCG 360
QY 409 ATCAATGTACAGGCTGTAATATGAGCGCGCAGCATAGCGAAGAAATTTGAAAGAA 468
Db 361 ATTATTTGCAACGAAATATGAGCGCAGCTTCTATGAGAAAGAAATATGAAAGAA 420
QY 469 TGTATATTGCCGAATTTAAACCTACAAATCATTTGAAGTGTATTTGAAGTGTACCGGA 528
Db 421 TGTATATTACCGCAATTTGAACCTATAAAATTTATGAAGGGGATTTGAAGTGTACCGGT 480
QY 529 GTTCAATTTATGATACACCGGCCATCTCCAGGCGATCAATCGCTATTAAATGAGACA 588
Db 481 GTTCAATTTATGATACCGCGAGTCAATCTCCAGGCCATCACTCGCTATTAAATGAGACA 540
QY 589 GAAAAATCCGCTCTGTTATTATTAACGATTTGATGATCGTATACGAAAGAAATTTTGA 648
Db 541 GAAAAATCCGCTCTGTTATTATTAACGATTTGATGATCGTATACGAAAGAAATTTTGA 600
QY 649 AATGAAGTGCCATTTGCGGGATTTGATTCAGAAATAGCTTTATCTCAATTAACGTTTA 708
Db 601 GATGAAGTGCCGTTGCGGGATTTGATTCGGAATTAGCTTTATCTCAATTAACGTTTA 660
QY 709 AAAGAAGTGGTGATCAAGAGAGAGCCGATGTTTCTTTTGACATGATATAGACAGGAA 768
Db 661 AAAGAAGTGGTGATCAAGAGAGAGCCAAATTTTCTTTGTCATGATATAGACAGGAA 720
QY 769 AGGGAGTGAAGTCTCCCTGAAATATATA 800
Db 721 AAGGGATTTAAAGTGTCCCTGAAATATATA 752
```

RESULT 5

ABK47470

ID ABK47470 standard; DNA; 753 BP.

XX AC

XX AC

XX AC

DT 29-AUG-2003 (revised)

DT 18-JUN-2002 (first entry)

XX XX

DE DE

DNA encoding autoinducer inactivation protein AiiE.

XX XX

XX KW

XX KW

XX KW

XX KW

XX OS

XX OS

XX FH

XX CDS

FT FT

FT FT

FT FT

XX XX

PN PN

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XX 28-FEB-2002.
PD 23-AUG-2000; 2000WO-SG000123.
XX PF 23-AUG-2000; 2000WO-SG000123.
XX PR 23-AUG-2000; 2000WO-SG000123.
XX PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX PI Zhang L, Dong Y, Xu J, Zhang H;
XX WPI; 2002-304123/34.
DR P-PSDB; AAU78806.
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
XX Claim 4; Fig 9; 82pp; English.
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably Bacillus thuringiensis which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.
CC This sequence encodes the autoinducer inactivation protein AiiE, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX SQ Sequence 753 BP; 243 A; 113 C; 173 G; 224 T; 0 U; 0 Other;
```

Query Match

51.0%; Score 623.4; DB 6; Length 753;

Best Local Similarity 89.2%; Pred. No. 2.le-123;

Matches 672; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

```
QY 49 ATGACAGTAAGAAGCTTTATTTTCGTCGCCAGCAGGTGTTGATGTTGGATCATTCGCT 108
Db 1 ATGACAGTAAGAAGCTTTATTTTCATCCAGCAGGTGTTGATGTTGGATCATTCGCT 60
QY 109 GTTAATAGTACATTAACACAGGAGAAATATTAGACTTACCGTTTGGTGTATCTTTTG 168
Db 61 GTTAACAGTGCCTTAACACCGGGGAAACTATTAAACTTGGCGGTGTTGTTATCTTTTG 120
QY 169 GAGACTGAAGAAGGACCTATTATTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT 228
Db 121 GAGACGGAAGAAGGCTCTATTATTAGTAGACACAGGTATGCCAGAAAGTGCAGTTAATAAT 180
QY 229 GAAGTCTTTTAAACGGTACATTTTCGAAGCGCAGGTTTACCGAAAATGACTGAAGAA 288
Db 181 GAAGGCTTTTAAACGGTACATTTTCGAAGCGCAGATTTTACCGAAAATGACTGAAGAA 240
QY 289 GATAGAAATCGTAATTTTAAACGGCTTGTATGAGCGGAGACCTTCTTTATATT 348
Db 241 GATAGAAATCGTAATTTTAAACGGCTTGTATGAGCGGAGACCTTCTTTATATT 300
QY 349 ATTAGTCTCACTTTCATTTTATGATCGACGAGGAAATGGCGCTTTTATAAATACACCA 408
Db 301 ATTAGTCTCACTTTCATTTTATGATCGACGAGGAAACGGTCTTTTACAATACACCA 360
QY 409 ATCAATGTACAGGCTGTAATATGAGCGCGCAGCATAGCGAAGAAATTTGAAAGAA 468
Db 361 ATTATTTGCAACGAAATATGAGCGCAGCTTCTATGAGAAAGAAATATGAAAGAA 420
QY 469 TGTATATTGCCGAATTTAAACCTACAAATCATTTGAAGTGTATTTGAAGTGTACCGGA 528
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Db 421 TGTATATTACCGCATTTGAACTACAAAATATTGTAAGGGATTATGAAGTGGTACCAGGT 480
QY 529 GTTCAATTATTGATACACAGGCCATACCTCCAGGGGATCAATCGCTATTAAATGAGACA 588
Db 481 GTTCAATTATTGATACACAGGCCATACCTCCAGGGGATCAATCGCTATTAAATGAGAGC 540
QY 589 GAAAAATCCGGTCTGTATTATTAAAGCAATGATCGATCGTATACGAAGAGAAATTTTGA 648
Db 541 GAGCAATCCGGTTCAGTTTTATTAAACGAATGATCGATCGTATACGAAGAGAAATTTTGA 600
QY 649 AATGAAGTGCATTTGCGGATTTGATTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 708
Db 601 GATGAAGTGCCTTCGAGATTTGATTCAGAAATAGCTTTATCTTCAATTAACAGTTTA 660
QY 709 AAGAAGTGTGTGATGAAGAGAGCCGATTTGTTTCTTTGGAATGATATAGCAGGAA 768
Db 661 AAGAAGTGTGTGAAGAGAGAAACCAATATTCTTTGTCATGATATAGCAGGAA 720
QY 769 AGGGGATGTAAGTGTTCCTCGATATATATAG 801
Db 721 AAGAGTTGTAGAGTGTTCCTCGATATATATAG 753

RESULT 6

ID ABK47469 standard; DNA; 753 BP.

XX AC ABK47469;

XX XX 29-AUG-2003 (revised)
DT DT 18-JUN-2002 (first entry)

XX DNA encoding autoinducer inactivation protein AiiD.

XX Autoinducer inactivation; AiiD; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; Erwinia carotovora; gene; ds.
XX

XX Bacillus thuringiensis; Bt.

XX Key Location/Qualifiers
FH 1..753
FT CDS /*tag= a
FT /*product= "AiiD"
FT /*note= "Autoinducer inactivation protein"

XX W0200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG000123.

XX 23-AUG-2000; 2000WO-SG000123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J, Zhang H;

XX WPI; 2002-304123/34.

XX P-PSDB; AAU78805.

PT Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.

XX Claim 4; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably

CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,
CC B17, B18, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiD, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)

XX Sequence 753 BP; 242 A; 113 C; 174 G; 224 T; 0 U; 0 Other;

QY Query Match 50.8%; Score 620.2; DB 6; Length 753;

QY Best Local Similarity 89.0%; Pred. No. 1e-122;
QY Matches 670; Conservative 0; Mismatches 83; Indels 0; Gaps 0;

QY 49 ATGACAGTAAGAAGCTTTATTTTCGCCAGCGAGTCTGTATGTTGGATCATTCGTCT 108
Db 1 ATGACAGTAAGAAGCTTTATTTTCATCCAGCAGTCTGTCATGTTGGATCATTCGTCT 60

QY 109 GTTAATAGTACATTAAACAGGAGATTTATAGACTTACCGTTTCGTTGTTATCTTTTG 168
Db 61 GTTAACAGTCTGTTAACACCGGGAACTATTAACTTGCCTGCTGTGTTATCTTTTG 120

QY 169 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAATAAT 228
Db 121 GAGACGGAAGAAGGTCCTATTTTAGTAGACACAGGTATGCCAGAAAGTGCAGTTAATAAT 180

QY 229 GAAGGTCTTTTAAACGGTACATTTTCGAAGGGCAGGTTTTTACCGAAATGACTGAAGAA 288
Db 181 GAAGGGCTTTTAAACGGTACATTTTGTGAAGGACAGATCTTACCGAAATGACTGAAGAA 240

QY 289 GATGAATCTGATATTTTAAACGGTGTGTTATGACGGGAGACCTCTTTATATT 348
Db 241 GATGAATCTGATATATTAAAGCGTGTGGGGTATGACGGGAGACCTCTTTATATT 300

QY 349 ATTAGTTCTCACTTGTCAATTTTGATCATGCAGGAGGAAATGGCGCTTTTATAATACACCA 408
Db 301 ATTAGTTCTCACTTGTCAATTTTGATCATGCAGGAGGAAACGGTCTTTACAATACACCA 360

QY 409 ATCAATCTACAGCGTCTGTAATATGAGCGGGCGCAGCATGCGGAAGAAATATTGAAAGAA 468
Db 361 ATTATTGTCAGCGAACCGAATATGAGCGACACTTCATAGAGAAGAAATATGAAAGAA 420

QY 469 TGTATATTGCGGAATTTAAACTCAAAATCAATTCGAAGTGATTAAGTCTGACCCAGGA 528
Db 421 TGTATATTACCGCATTTTGAACACTACAAAATTTATTGAAGGGGATTTGAAGTGTGACCGGT 480

QY 529 GTTCAATTTATTGCATACACAGGCGCATCTCCAGGGCATCAATCGCTATTAAATTGAGACA 588
Db 481 GTTCAATTTATTGTATAGCCAGGTCACTTCAGGCGCATCAATCGCTATTAAATTGAGAGC 540

QY 589 GAAAAATCCGGTCTCTGTATTATTAAACGATTCGATCGTATAGAAAGAGAAATTTTGA 648
Db 541 GAGCAATCCGGTTCAGTTTTATTAAATGATTCATCGTACACGAGAAAGAGAAATTTTGA 600

QY 649 AATGAAGTGCATTTGCGGGATTTGATTCAGAAATAGCTTTATCTTCAATTAAGCTTTTA 708
Db 601 GATGAAGTGCCTTCGCGAGGATTTGATCCAGAAATAGCTTTATCTTCAATTAAGCTTTTA 660

QY 709 AAAGAAGTGTGTGATGAAGAAGAGCCGATTTCTTTTGGACATGATATAGCAGGAA 768
Db 661 AAAGAAGTGTGAAGAAGAGAGAACCAATTTATTTCTTTGTCATGATACAGCAGGAA 720

QY 769 AGGGATGTAAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGAGTTGTAGAGTGTTCCTCGAATATATATAG 753

RESULT 7

ID ABK47474

standard; DNA; 753 BP.

PR 23-AUG-2000; 2000WO-SG000123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX Zhang L, Dong Y, Xu J, Zhang H;
XX WPI; 2002-304123/34.
DR P-PSDB; AAU78809.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
PT
XX
XX Claim 4; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiJ, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
XX
XX Sequence 753 BP; 235 A; 111 C; 176 G; 231 T; 0 U; 0 Other;
SQ

Query Match 50.5%; Score 617; DB 6; Length 753;
Best Local Similarity 88.7%; Pred. No. 4.9e-122;
Matches 668; Conservative 0; Mismatches 85; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAGAAGCTTTATTCGTCGCCAGCGTGGTTGATGTTGGATCATTCGTCT 108
Db 1 ATGACAGTAAGAAGCTTTATTCATCCAGCAGGTCGTTGTATGTAGATCATTCCTCT 60

Qy 109 GTTAAATAGTACATTAACACGAGGAATATTAGACTTACCGTTTCGTTGTTACTTTTG 168
Db 61 GTTAAATAGTACACTCGCGCGCGGGAATTTATGAACTTACCTGATGTTGTTACTTTTG 120

Qy 169 GAGACTGAAGAAGGACCTATTATTAGTAGATACAGTATGCCAGAAAGTCAGTTAATAAT 228
Db 121 GAGACAGAGNAGGCGCTATTATTAGTAGATACAGTATGCCAGAAAGTCAGTTAATAAT 180

Qy 229 GAAGGTCCTTTTAAACGGTACATTTGTGGAAGGGCAGGTTTACCGAAATGACTGAAGAA 288
Db 181 GAAGGCTCTTTTAAACGGTACATTTGTGGAAGGACAGATTTTACCGAAATGACTGAAGAA 240

Qy 289 GATAGATCGTGAATTTTAAACGGTTCGTTATGACCGGAGACCTCTCTTTATATT 348
Db 241 GATAGATCGTGAATTTTAAACGGTTCGTTATGACCGGAGACCTCTCTTTATATT 300

Qy 349 ATTAGTCTCTCACTTTCATCTTTGATCATGCAGAGGAAATGCGCTTTTATAATACACCA 408
Db 301 ATTAGTCTCTCACTTTCATCTTTGATCATGCAGAGGAAACGGTCTTTTACAAATACACCG 360

Qy 409 ATCATTTGACGCTGCTGAATATGAGCGCGCGAGCATAGCGAAGATATTGGAAGAA 468
Db 361 ATTATTGTGACGCGAGCGGAATATGAGCGAGCACTTTCATAGAGAGAATATATGAAGAA 420

Qy 469 TGTATTATGCGGAATTTAACTACAAATCATTTGAAGGTGATTATGAAGTCTGACAGGA 528
Db 421 TGTATTATGCGCAATTTGAATCATCAAAATTTATGAAGGGATTATGAAGTGTACACAGT 480

Qy 529 GTTCAATTATTGCATACACCGCGCATCTCCAGGGCATCAATCGCTATTATTCAGACA 588
Db 481 GTTCAATTATTGTATACGCCAGGTCACTTCTCAGGCCATCAGTCGTTATTTCATTGAGACG 540

Qy 589 GAAAAATCCGTCCTCTGTTATTATTAAAGATTGATGCATCGTATACGAAGAGAAATTTTGAA 648
Db 541 GAGCAATCCGGTTTCAGTTTTTATTAACAATTGATGCATCGTACACGAAGAGAAATTTTGAA 600

Qy 649 AATGAAGTGCCATTTTCGGGATTTGATTCAGAATTAGCTTTTATCTTCAATTAACCGTTTA 708
Db 601 GATGAAGTGCCGTTTCGACGAGATTGATCCAGAAATAGCTTTTATCTTCAATCAACGTTTA 660

Qy 709 AAAGAAAGTGATGATGAAGAAAGAGCCGATTTGTTTCTTTGACATGATATAGACAGGAA 768
Db 661 AAAGGAGTTGTGCGGGAAGAGAAACCAATTTGTTTCTTTGTCATGATATAGACAGGAA 720

Qy 769 AGGGGATGTAAAGTGTTCCTCGATATATATAG 801
Db 721 AAGGGTTGTAGAGTGTTCCTCGATATATATAG 753

RESULT 9
ABK47475
ID ABK47475 standard; DNA; 753 BP.
XX
XX AC ABK47475;
XX
XX 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)
XX
XX DNA encoding autoinducer inactivation protein AiiJ.
DE
XX Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*; gene; ds.
XX
XX *Bacillus thuringiensis*; B22.
OS
XX
XX Key Location/Qualifiers
FH 1..753
FT CDS /*tag= a
FT /product= "AiiJ"
FT /note= "Autoinducer inactivation protein"
XX
XX WO200216623-A1.
XX
XX 28-FEB-2002.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX
XX 23-AUG-2000; 2000WO-SG000123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
XX Zhang L, Dong Y, Xu J, Zhang H;
PI
XX WPI; 2002-304123/34.
DR P-PSDB; AAU78811.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
XX
XX
XX Claim 4; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis*, which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC

CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiK, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 753 BP; 234 A; 111 C; 177 G; 231 T; 0 U; 0 Other;

Query Match 50.4%; Score 615.4; DB 6; Length 753;
Best Local Similarity 88.6%; Pred. No. 1.1e-121;
Matches 667; Conservative 0; Mismatches 86; Indels 0; Gaps 0;

QY 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGGTCGTGTATGTTGGATCATTCGTCT 108
Db 1 ATGACAGTAAAGAGCTTTATTTTCATCCAGCAGGTCGTGTATGTTAGATCATTCCTCT 60
QY 109 GTTAATAGTACATTAAACACGAGAGATTTATAGACTTACCGGTTTGGTGTATCTTTTG 168
Db 61 GTTAATAGTACACTCGCGCGGGGAATTTATTGAACCTTACCTGATGGTGTATCTTTG 120
QY 169 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 228
Db 121 GAGACAGAAGAGGGGCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 180
QY 229 GAAGGTCCTTTTAAACGCTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAA 288
Db 181 GAAGGGCTTTTAAACGCTACATTTGTTGAAGGACAGATTTTACCAGAAATGACTGAAGAA 240
QY 289 GATAGAATCGTGAATATTTTAAACGGGTTGTTATGAGCGGGAAGACCTTCTTTATATT 348
Db 241 GATAGAATCGTGAATATTTAAAGCGGTAGGATGAGCGGAGACCTTTTATATATT 300
QY 349 ATTAGTCTCATTGCACTTTTGTATGATGAGGAGGAAATCGCGGTTTATAAATACACCA 408
Db 301 ATTAGTCTCATTGCACTTTTGTATGATGAGGAGGAAACGGTCTTTTACAAATACACCG 360
QY 409 ATCAATTGTACAGCGTCTGAATATGAGCGGCGCCAGCATAGCGAAGATATTTGAAGAA 468
Db 361 ATTATTTGTGAGCGAGCGGGAATATGAGCGAGCACTTCTATGAGAAGATATATGAAGAA 420
QY 469 TGTATATTGCGGAATTTAAACTACAAATCATTTGAAGGTCATTTGAAGTCGTACACGGA 528
Db 421 TGTATATTACCGCATTTGAACATAAAATTTATTGAAGGGAATTTAGAGTGGTACACGGT 480
QY 529 GTTCAATATTGATATACACAGCGCATATCCAGGCGATCAATCGGTATTAATGAGACA 588
Db 481 GTTCAATATTGATATACAGCGCATATCTCCAGGCGCATCAGTCGTATTTCATTGAGACG 540
QY 589 GAAAAATCCGGTCTCTGATTTAATTAACGATGATGATCGATATACGAAGAGAAATTTGAA 648
Db 541 GAGCAATCCGGTTCAGTTTATTAAATGATGATGATGATGATGATGATGATGATGATGAA 600
QY 649 AATGAAGTGCCATTTGCGGGAATTTGATTTCAAGATTTAGCTTTTATCTTCAATTAACGTTT 708
Db 601 GATGAAGTGCCGTTGCGAGGATTTGATCCAGAAATTTAGCTTTTATCTTCAATCAACGTTT 660
QY 709 AAGAAGTGTGATGAAGAAGAGCGGATGTTTCTTGGACATGATATAGAGAGGAA 768
Db 661 AAGAAGTGTGCGGGAAGAGAAACCAATTTGTTTCTTGGTATGATATAGAGAGGAA 720
QY 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGGGTTGATAGTGTTCCTCGAATATATATAG 753

RESULT 10
ABK47476
ID ABK47476 standard; DNA; 753 BP.
XX
AC ABK47476;
XX
DT 29-AUG-2003 (revised)
DT 18-JUN-2002 (first entry)

XX DNA encoding autoinducer inactivation protein AiiK.
DE Autoinducer inactivation; AiiK; N-acyl-homoserine lactone;
XX disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*; gene; ds.
XX
OS *Bacillus thuringiensis*; B25.
XX
FH Key Location/Qualifiers
FT CDS 1..753
FT /tag= a
FT /product= "AiiK"
FT /note= "Autoinducer inactivation protein"
XX
PN MO200216623-A1.
XX
PD 28-FEB-2002.
XX
PF 23-AUG-2000; 2000WO-SG000123.
XX
PR 23-AUG-2000; 2000WO-SG000123.
XX
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX
PI Zhang L, Dong Y, Xu J, Zhang H;
XX
DR WPI; 2002-304123/34.
DR P-PSDB; AAU78812.
XX
PT Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to a
PT disease in sustainable plant or animal and for reducing bacterial damage.
XX
PS Claim 4; Fig 9; 82pp; English.
XX
CC The invention describes an isolated polynucleotide encoding an
CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This sequence encodes the autoinducer inactivation protein AiiK, the
CC autoinducer inactivation activity of which is studied in the invention.
CC (Updated on 29-AUG-2003 to standardise OS field)
XX
SQ Sequence 753 BP; 236 A; 110 C; 176 G; 231 T; 0 U; 0 Other;

Query Match 50.2%; Score 613.8; DB 6; Length 753;
Best Local Similarity 88.4%; Pred. No. 2.4e-121;
Matches 666; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 49 ATGACAGTAAAGAGCTTTATTTTCGTCGCCAGCAGGTCGTGTATGTTGGATCATTCGTCT 108
Db 1 ATGACAGTAAAGAGCTTTATTTTCATCCAGCAGGTCGTGTATGTTAGATCATTCCTCT 60
QY 109 GTTAATAGTACATTAAACACGAGAGATTTATAGACTTACCGGTTTGGTGTATCTTTTG 168
Db 61 GTTAATAGTACACTCGCGCGGGGAATTTATTGAACCTTACCTGATGGTGTATCTTTG 120
QY 169 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 228
Db 121 GAGACAGAAGAGGGGCTATTTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 180
QY 229 GAAGGTCCTTTTAAACGCTACATTTGTCGAAGGCGAGGTTTACCAGAAATGACTGAAGAA 288

Db 181 GAAGGCTTTTAAACGCTACATTTGTTGAGGACAGATTTTACCGAAATGACTGAAGAA 240
 QY 289 GATAGAAATCGTGAATATTTTAAACGGTGTGTTATGAGCCGGAAGACCTCTTTATATT 348
 Db 241 GATAGAAATCGTGAATATTTAAAGCGTGTAGGCTATGAGCCGACACCTTTTATATATT 300
 QY 349 ATTAGTTCTCAGTTCATTTGATCATGACGAGGAAATGGCGCTTTTAAATACACCA 408
 Db 301 ATTAGTTCTCAGTTCATTTGATCATGACGAGGAAATGGCGCTTTTAAATACACCA 360
 QY 409 ATCAATGTACAGCGTCTCAATATGAGCGCGCCAGCATAGCAGAAATATTTGAAGAA 468
 Db 361 ATTATGTGAGCGAAGCAATATGAGCGACGACTTATAGAGAAATATATGAAGAA 420
 QY 469 TGATATTCGCGAATTTAACTACAAATCAATTAAGAGTGATTAAGTCGTACAGGA 528
 Db 421 TGATATTCGCGAATTTAACTACAAATCAATTAAGAGTGATTAAGTCGTACAGGA 480
 QY 529 GTTCAATTTATGATACACAGCGCCATCTCCAGGGCATCAATCGCTATTATTTGAGACA 588
 Db 481 GTTCAATTTATGATACAGCGCGCATCTCCAGGGCATCAATCGCTATTATTTGAGACA 540
 QY 589 GAAAAATCCGGTCTCTGATTTATTAAGCAATGATGCTATACGAAAGAGAAATTTTGA 648
 Db 541 GACCAATCCGGTTCAGTTTATTAACAATGATGCTATACGAAAGAGAAATTTTGA 600
 QY 649 AATGAAGTGCATTTGCGGGAATTTGATTCAGAAATAGCTTTTATCAATTAACGTTTA 708
 Db 601 GATGAAGTGCATTTGCGGGAATTTGATTCAGAAATAGCTTTTATCAATTAACGTTTA 660
 QY 709 AAGAAAGTGGTATGAAGAGAGAGCCGATGTTTCTTGGACATGATATAGAGCAGGA 768
 Db 661 AAGAGGAGTGTGCGGAAAGAGAAACCAATTTGTTCTTGGTATGATATAGAGCAGGA 720
 QY 769 AGGGAGTGAAGAGTTCCTCGAATATATATAG 801
 Db 721 AAGGGTGTAGAGTGTCTCGATATATATAG 753

RESULT 11
 ABZ10246
 ID ABZ10246 standard; DNA; 8056 BP.
 AC ABZ10246;
 XX
 XX
 16-JAN-2003 (first entry)
 XX
 XX
 Haematopoietic cell proliferation disorder related DNA sequence #386.
 DE
 DE
 KW Human; haematopoietic cell proliferation disorder; cytostatic;
 KW Gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia;
 KW cytosine methylation state; gene; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX
 DN W0200277272-A2.
 PD
 PD 03-OCT-2002.
 XX
 XX 26-MAR-2002; 2002WO-EP003401.
 XX
 XX 26-MAR-2001; 2001US-0278333P.
 PR
 XX (EPIG-) EPIGENOMICS AG.
 PA
 XX Berlin K, Braun A, Distler J, Guetig D, Howe A, Mueller J;
 PI Olek A, Piepenbrock C, Adoxjan P, Grabs G, Lesche R, Leu B;
 PI Lewin A, Lipscher B, Maier S, Model F, Mueller V, Otto T, Pelet C;
 PI Schwabe I, Ziebarth H;
 XX
 XX WPI; 2003-018942/01.
 DR
 XX
 XX Detecting and differentiating between hematopoietic cell proliferative

PT disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides.
 PT
 XX Claim 28; SEQ ID NO 386; 117pp; English.
 XX
 CC The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention can be used: for differentiating between healthy haematopoietic cells and proliferative disorder haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation disorder related DNA sequences. The nucleotide sequences from the present invention can also be used for detecting a predisposition to, differentiation between subclones, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders allowing for improved and informed treatment of patients

XX
 SQ Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 U; 0 Other;

Query Match 4.7%; Score 57; DB 7; Length 8056;
 Best Local Similarity 47.4%; Pred. No. 0.017;
 Matches 171; Conservative 0; Mismatches 190; Indels 0; Gaps 0;

QY 836 TTTCGTTTAAAGCATTTTAAATAGTTATTAACCTTTTAAAGACTATCTTCATTTAA 895
 Db 1080 TTTGTTTTTTTTTAAATGTTTTAAATGTTATATATTTGTTTTTAAATTTTGTAT 1139
 QY 896 TTGATAGTACGTAAAGTTTACATCATTTAGGAGTATCTGTTGAGCAATCATCTCGTT 955
 Db 1140 ATTGAAATTTTAAATTAATATATTTTGGATTTATTAATTTTAAATTTTAAATTTAAT 1199
 QY 956 ACTGTGATGTCACCTACCATATGAAATATTTTTTATAAGTCCCATCTCGAAAGTAAT 1015
 Db 1200 ATTTATTTAATTTTAAATTTTAAATTAATAATTTTGTGAATAAAAAAATGTTAT 1259
 QY 1016 CCACATATCACAGTCTATTAATCTGATCTCTTCATCTAATGTTAAATTTCTCTTTT 1075
 Db 1260 GTAAATTAATTAATAATAAAAAATGTAATTTTTTAAAAAATTAATAAATAAAAA 1319
 QY 1076 GCGGGTATCCATCTGTTAATGATGTTTTTAAATTCATCTGTTTCTGAGAAAGATATC 1135
 Db 1320 TTTATTAATAATTTTAAATAAAAAATTAATTTAAATTTTAAATTTTAAATTTTATTT 1379
 QY 1136 CTTTGTGTTTTTAAATGACTCGACATGATATCTTTTATTTCTTGTTTCTCTAAAGAGAC 1195
 Db 1380 TTTTATTAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATAATA 1439
 QY 1196 A 1196
 Db 1440 A 1440

RESULT 12
 AAS46334
 ID AAS46334 standard; DNA; 7667 BP.
 XX
 XX AAS46334;
 AC
 XX
 XX 18-DEC-2001 (first entry)
 DT
 XX Tumour suppressor gene derived chemically modified sequence #56.
 DE
 XX

KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic; cancer;
 KW tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
 KW cytosine methylation; ds.

XX Homo sapiens.

XX WO200168912-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-EP002955.

XX 15-MAR-2000; 2000DE-01013847.

XX 06-APR-2000; 2000DE-01019058.

XX 07-APR-2000; 2000DE-01019173.

XX 30-JUN-2000; 2000DE-01032529.

XX 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-602752/68.

XX Fragments of chemically modified genes associated with tumor suppressor
 PT genes and oncogenes, useful in designing primers and probes for analyzing
 PT diseases associated with cytosine methylation state e.g. cancer.

XX Claim 1; SEQ ID NO 56; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18
 CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
 CC bisulphite, of genes associated with tumour suppression and oncogenes
 CC having a sequence taken from 536 (actually 533 since numbers 408, 458 and
 CC 500 are missing from the sequence listing) sequences (Ss) and sequences
 CC complementary to (Ss). The nucleic acid may be a peptide nucleic acid-
 CC oligomer (PNA) of at least 9 nucleotides and may form part of a set of
 CC probes for detecting the cytosine methylation state and/or single
 CC nucleotide polymorphisms and also to be used in an array for analysing
 CC diseases associated with CpG dinucleotides e.g. cancers and tumours. The
 CC probes can also be used in a method for ascertaining genetic and/or
 CC epigenetic parameters for the diagnosis and/or therapy of existing
 CC diseases or the predisposition to specific diseases, by analysing
 CC cytosine methylations. The parameters may be compared to another set of
 CC genetic and/or epigenetic parameters, the differences serving as basis
 CC for diagnosis and/or prognosis events which are disadvantageous to
 CC patients. The present sequence is one of the 533 genomic sequences
 CC derived from tumour suppressor genes and oncogenes. Sequences with even
 CC numbered Seq ID numbers are the complementary sequence of the
 CC corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID
 CC 535, except for those whose partner sequence is missing). Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 7667 BP; 2292 A; 63 C; 1436 G; 3876 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 4.6%; Score 56.6; DB 4; Length 7667;

XX Matches 176; Conservative 0; Mismatches 199; Indels 0; Gaps 0;

QY 820 TATTCGCTCATGACTTTTCGTTAAATGATTTTTTAAATAAGTATTAACCTTTTAG 879

DB 4585 TATTTTATGTTTATTTTAAATTTTATTTTAAATTTTATTTTATTTTGGTTAGATT 4644

QY 880 AACTATCTTCATTTAATGTAGTACGTAAGGTTTACATCATTAGGAGTATCTGTTGAG 939

DB 4645 AGTTGTTTATTAATATATTAGTATTATTTTATTTTATTTTATTTTATTTTATTAAG 4704

QY 940 CAATCATCATCTCGTTACTGTGATGGTCAACTACCCATATCAATATTTTATAAGTCC 999

DB 4705 GTTTGTTTATGTTTATTTTGGTGGTTTCTATTTTATTTTATTTGATTATTTGATT 4764

QY 1000 CATCCTCGAAAGTAATCCACATATCAGAGTCTATTAAATCTGATCCTTCTTCATCTAATG 1059
 DB 4765 TTTAAGTAGTTTTTATTGATTGTTTAGTTGTTAAATTTTTTTTTTTTTTTTTTTCGT 4824
 QY 1060 TTAATTTTCCTTTTTTTGGCGGTATCCATACCTGTTAAATGAATGTTTAAATTCATCTGTTT 1119
 DB 4825 TTAATAATAGTATTTTTTTTGTATTTTTTTTGAAGAAGTATTTTTTATTTATATTT 4884
 QY 1120 TTGTGAGAAAGATATCCTTTTTTCTTTTAAATGTAGTACGATGATATATCTTTTATTTCTT 1179
 DB 4885 TTTATTTTGAATATTTTGTGTTGTTTAAATTTATTTGATTGTTATATTTTATTTAT 4944
 QY 1180 GTTTTCTCTAAAAACA 1194
 DB 4945 TTTTATTTTAAATAAGA 4959

RESULT 13

ABL32267

ID ABL32267 standard; DNA; 6419 BP.

XX AC ABL32267;

XX DT 26-MAR-2002 (first entry)

XX DE Human immune system associated gene SEQ ID NO: 240.

XX KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianaemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmologic;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 ds.

XX OS Homo sapiens.

XX WO200200928-A2.

XX 03-JAN-2002.

XX 02-JUL-2001; 2001WO-EP007537.

XX 30-JUN-2000; 2000DE-01032529.

XX 01-SEP-2000; 2000DE-01043826.

XX (EPIG-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2002-130909/17.

XX Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.

XX Claim 1; SEQ ID NO 240; 32pp + Sequence Listing; German.

XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention

XX SQ Sequence 6419 BP; 1565 A; 53 C; 1453 G; 3348 T; 0 U; 0 Other;

XX Query Match

XX Best Local Similarity 4.5%; Score 55.6; DB 6; Length 6419;

XX Matches 195; Conservative 0; Mismatches 214; Indels 1; Gaps 1;

CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention
 XX
 SQ Sequence 14006 BP; 3278 A; 155 C; 3257 G; 7313 T; 0 U; 3 Other;
 Query Match 4.5%; Score 55.6; DB 6; Length 14006;
 Best Local Similarity 47.0%; Pred. No. 0.038;
 Matches 172; Conservative 0; Mismatches 194; Indels 0; Gaps 0;
 QY 819 TTATTTCGTCATGACATTTTCGTTAAATGATTTTTTTAAATAGTTATAAACTTTTTTA 878
 Db 1995 TTTTTCGTTTCGATT 2054
 QY 879 GAACATATCTTCATTTAAATGATAGTAGTAAGGTTTACATCATTAGGAGTATCTGTGTA 938
 Db 2055 TTTTTCGTTTCGATT 2114
 QY 939 GCAATCATCACTTCGTTTACTGATGATGTCACCTACCCATATGAAATATTTTATAAGTC 998
 Db 2115 TTTTTCGTTTCGATT 2174
 QY 999 CCATCTCGAAAGTAATCCACATATCACAGTCTATTAAATCTGATCCTCTTCATCTAAT 1058
 Db 2175 TTTTTCGTTTCGATT 2234
 QY 1059 GTTAAATTTTCCTTTTTTGGCGGTATCCATCTACTGTAAATGAATGTTTAAATTCATCTGT 1118
 Db 2235 TTTTTCGTTTCGATT 2294
 QY 1119 TTGTGAGAAAGATATCCCTTTTTTGTGTTTAAATGACTCGACATGATATCTTTTATTTCT 1178
 Db 2295 TTTTTCGTTTCGATT 2354
 QY 1179 TGTGTTT 1184
 Db 2355 TTTTTC 2360
 RESULT 15
 ABK31511
 ID ABK31511 standard; DNA; 47108 BP.
 XX
 AC ABK31511;
 XX
 DT 23-APR-2002 (first entry)
 XX
 DE Signal transduction associated gene modified complementary DNA #177.
 XX
 KW Human; signal transduction associated gene; cytosine methylation state;
 KW CpG island; signal transduction associated disease; solid tumour; cancer;
 KW antitumour; cytostatic; mutant; ds.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 PN WO200200926-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-EP007472.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 CC

775 TGFAAGTGTCCCTGAATATATATAGTACAAAAGTCATGACCTTATTCGTCATGACT 834
 Db 1571 TTTTTCGTTTCGATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTATTT 1630
 QY 835 TTTTCGTTTAAAGATTTTTTAAATAAGTTATAAACTTTTTTAAAGTATCTTCATTVA 894
 Db 1631 TATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTA 1690
 QY 895 AATGATAGTACGTAAGGTTTACATCATTAGGAGTATCTTGTTCGAGCAATCA-TCACCTCG 953
 Db 1691 TTTTTCGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 1750
 QY 954 TTACTGTGATGTCACATCCCATATGAATATTTTTTAAAGTCCCATCTCGAAGATA 1013
 Db 1751 TTATTTATTTTATTTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 1810
 QY 1014 ATCCACATATCACAGTCTATTAAATCTGATCCTCTTCATCTAATGTTATTTTCCTTTT 1073
 Db 1811 TTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTATTTAT 1870
 QY 1074 TTGCGGTATCCATCTGTTTAATGAATGTTTTTAAATCATCTGTTTGTGAGAAAGATA 1133
 Db 1871 TTATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTG 1930
 QY 1134 TCCTTTTCGTTTAAATGACTCGACATGATATCTTTTATTTTCCTTTCTGTTT 1183
 Db 1931 TTGTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTCTGTTT 1980
 RESULT 14
 ABL33958
 ID ABL33958 standard; DNA; 14006 BP.
 XX
 AC ABL33958;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human immune system associated gene SEQ ID NO: 1931.
 XX
 KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antianemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antididiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease; gene;
 KW ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 PD 03-JAN-2002.
 XX
 PF 02-JUL-2001; 2001WO-EP007537.
 XX
 PR 30-JUN-2000; 2000DE-01032529.
 PR 01-SEP-2000; 2000DE-01043826.
 XX
 PA (EPIG-) EPIGENOMICS AG.
 XX
 PI Olek A, Piepenbrock C, Berlin K;
 XX
 DR WPI; 2002-130909/17.
 XX
 PT Nucleic acid comprising fragment of chemically modified gene, useful for
 PT diagnosis and treatment of diseases associated with abnormal cytosine
 PT methylation.
 XX
 PS Claim 1; SEQ ID NO 1931; 32pp + Sequence Listing; German.
 XX
 CC The present invention provides a number of human immune system associated

DR WPI; 2002-147896/19.

XX Oligonucleotide for diagnosis and therapy of diseases associated with

PT signal transduction e.g. cancer, comprises chemically modified genomic

PT sequences of genes associated with signal transduction.

XX

PS Claim 1; SEQ ID NO 354; 24pp; English.

XX

CC The present invention relates to chemically modified DNA sequences of

CC signal transduction associated genes. The DNA sequences are chemically

CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.

CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting

CC the cytosine methylation state (CpG islands) of these genes, and a method

CC for the diagnosis and/or therapy of genetic and epigenetic parameters of

CC genes associated with signal transduction. The genomic DNA can be

CC obtained from cells or cellular components which contain DNA, e.g. cell

CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,

CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,

CC brain, heart, prostate, lung, breast or liver, histologic object slides,

CC and all their possible combinations. The sequences of the invention are

CC useful for the diagnosis and therapy of diseases associated with signal

CC transduction e.g. solid tumours and cancer. ABK31158-ABK31545 represent

CC chemically pretreated genomic DNA sequences of different genes associated

CC with signal transduction, or their complementary sequences. Note: The

CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the

CC European Patent Office

XX

SQ Sequence 47108 BP; 15349 A; 429 C; 8736 G; 22594 T; 0 U; 0 Other;

Query Match 4.5%; Score 55.6; DB 6; Length 47108;

Best Local Similarity 45.2%; Pred. No. 0.046;

Matches 205; Conservative 0; Mismatches 249; Indels 0; Gaps 0;

QY 736 ATTGTTTCTTTGGACATGATATAGACGAGGAAGGGGATGTAAGTGTTCCTGGAATAT 795

Db 40450 ATGATATTTAAAGGAACGAATTTTAAATTTGGGGGTGTTAATTAGTTGGTAGTAA 40509

QY 796 ATATAGTACAAAAGTCATGAGCTTATCGCTCAGACTTTTTCGTTTAAATGATTTTTT 855

Db 40510 ATATTTTAAATTCGAAAAATTTGGAATTTTAAATATTTTGGTTTAAAGTTTGA 40569

QY 856 TAAATAGTTTAAACATTTTGTAGAACTATCTTCATTTAATTGATAGTACGTAAGTTTA 915

Db 40570 TAAGGGTTATTTAAATTTGTATATTAATTTTAAATGTTTAGTTATATATGATGATTA 40629

QY 916 CATCATTAGGAGTATCTTTGTGAGCAATCATCACTTCGTTACTGTGATGGTCAACTACCC 975

Db 40630 TATTTTAAATAAATATTTTATTTTAAAGTGTAAATGTTTAAAGATATATTAAGATTA 40689

QY 976 ATATGAATATTTTATATAGTCCCATCCCGAAAGTAATCCACATATCACAGTCTAATA 1035

Db 40690 ATGTAATATTTTATATATTTTAAAGATTTTGTGATTATTTAATTATTTATTATT 40749

QY 1036 AATCTGATCCTTCTCATCTAATGTTAATTTTCCTTTTGGGGGTATCCATAGCTGTAA 1095

Db 40750 TTTTAAAGTTTATTAATAAATAAATAAATAATAGATGTTTTTGGTATGAAATTTGTAG 40809

QY 1096 TGAATGTTTTTAATCATCTGTTTTTGTGAGAAAGATATCCTTTTGTGTTTAAATGACT 1155

Db 40810 TCGAGATTTTATTTTGGTGGTAGATTTATGTTTGGATTTTAAATTTTAAATTTTAA 40869

QY 1156 CGACATGATATCTTTTATTTCTGTTTCTTAA 1189

Db 40870 ACGAATTTAAATGATTTTTTTTGTGATTTTAA 40903

Search completed: February 24, 2004, 02:43:29

Job time : 419 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 24, 2004, 01:04:17 ; Search time 3429 Seconds

(without alignments)
15446.249 Million cell updates/sec

Title: US-10-019-661-1

Perfect score: 1222

Sequence: 1 ctttactgtattgttttatt.....tcatttgggtctctttgagt 1222

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

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9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

32: em_htg_other.*

33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_mam.*

37: em_htg_vrt.*

38: em_sy.*

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40: em_htgo_mus.*

41: em_htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1222	100.0	1222	1	AF196486	AF196486 Bacillus
2	1222	100.0	1222	6	AX068093	AX068093 Sequence
3	1037	84.9	1339	1	AF350927	AF350927 Bacillus
4	1037	84.9	1339	6	AX391415	AX391415 Sequence
c	1032.2	84.5	312049	1	AE017035	AE017035 Bacillus
c	1018.8	83.4	301665	1	AE017009	AE017009 Bacillus
7	980.2	80.2	1369	1	AY460124	AY460124 Bacillus
8	729	59.7	753	1	AF397400	AF397400 Bacillus
9	687.4	56.3	753	1	AF478058	AF478058 Bacillus
10	677.8	55.5	753	1	BAC505742	AF478058 Bacillus
11	644.2	52.7	753	1	AF350931	AF350931 Unculture
12	644.2	52.7	753	6	AX391419	AF350931 Bacillus
13	634.2	51.9	753	1	AF478052	AX391419 Sequence
14	633.6	51.8	753	1	AF350930	AF478052 Bacillus
15	633.6	51.8	753	6	AX391418	AF350930 Bacillus
16	633	51.8	753	1	AF478056	AX391418 Sequence
17	628.2	51.4	753	1	AF195570	AF478056 Bacillus
18	625	51.1	753	1	AF478046	AF195570 Bacillus
19	625	51.1	753	1	AF478048	AF478046 Bacillus
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21	625	51.1	753	1	AF478057	AF478053 Bacillus
22	623.4	51.0	753	1	AF350929	AF478057 Bacillus
23	623.4	51.0	753	1	AF478051	AF350929 Bacillus
24	623.4	51.0	753	6	AX391417	AF478051 Bacillus
25	621.8	50.9	753	1	AF478045	AX391417 Sequence
26	621.8	50.9	753	1	AF478050	AF478045 Bacillus
27	621.8	50.9	753	1	AF478059	AF478050 Bacillus
28	620.2	50.8	753	1	AF350928	AF478059 Bacillus
29	620.2	50.8	753	1	AF195571	AF350928 Bacillus
30	620.2	50.8	753	1	AF198412	AF195571 Bacillus
31	620.2	50.8	753	1	AX332611	AF198412 Bacillus
32	620.2	50.8	753	6	AX391416	AX332611 Sequence
33	618.6	50.6	753	1	AF478061	AX391416 Bacillus
34	617	50.5	753	1	AF350932	AF478061 Bacillus
35	617	50.5	753	1	AF350933	AF350932 Bacillus
36	617	50.5	753	1	AF478060	AF350933 Bacillus
37	617	50.5	753	6	AX391420	AF478060 Bacillus
38	617	50.5	753	6	AX391421	AX391420 Sequence
39	615.4	50.4	753	1	AF350934	AX391421 Sequence
40	615.4	50.4	753	1	AF478047	AF350934 Bacillus
41	615.4	50.4	753	1	AF478049	AF478047 Bacillus
42	615.4	50.4	753	6	AX391422	AF478049 Bacillus
43	613.8	50.2	753	1	AF350935	AX391422 Sequence
44	613.8	50.2	753	1	AF478054	AF350935 Bacillus
45	613.8	50.2	753	6	AX391423	AF478054 Bacillus

ALIGNMENTS

RESULT 1
AF196486
LOCUS AF196486
DEFINITION Bacillus sp. 240B1 putative metallohydrolase (aiia) gene, complete cds.
Bacillus sp. 240B1
Bacillus sp. 240B1
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
Dong, Y.H., Xu, J.L., Li, X.Z. and Zhang, L.H.
AiiA, an enzyme that inactivates the acylhomoserine lactone
quorum-sensing signal and attenuates the virulence of *Erwinia*

ACCESSION AF196486
VERSION AF196486.1
KEYWORDS GI:7416988
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 1222)
AUTHORS
TITLE

Pred. No. is the number of results predicted by chance to have a

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	Ddb	601	CTGTATTATTAAACGATTGATCGATCGTATACGAAGAAGAAATTTTGAAAATGAAGTGCCA	660
	Qy	661	TTTGGGGATTGATTCAGAAATTAGCTTTATCTTCAAATTAAGCGTTTTAAAGAGAGTCGGT	720
	Ddb	661	TTTGGGGATTGATTCAGAAATTAGCTTTATCTTCAAATTAAGCGTTTTAAAGAGAGTCGGT	720
	Qy	721	ATGAAGAAGAACCGCATCTTTCTTTGGACATGATATAGACGAGGAGGAGGATGTAAA	780
	Ddb	721	ATGAAGAAGAACCGCATCTTTCTTTGGACATGATATAGACGAGGAGGAGGATGTAAA	780
	Qy	781	GTTGTTCCCTGAATPATATATAGTACAAAAAGTCAAGAGCTTATTCCGTCATGACTTTTTCG	840
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	Qy	841	TTTAAATGATTTTTTAAATTAAGTATAAATTTTTTTAGAACTATCTTCAATTTAAATGAT	900
	Ddb	841	TTTAAATGATTTTTTAAATTAAGTATAAATTTTTTTAGAACTATCTTCAATTTAAATGAT	900
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	Ddb	901	AGTACGTAAGGTTTACATCATTTAGGAGTATCTTTGTAGCAATCATCACCTTCGTTACTGT	960
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	Ddb	1021	TATCACAGTCTATTAATCTGATCCCTCTTCATCTAATGTTAAATTTTCCTTTTTTGGCGG	1080
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	Ddb	1201	GCTCAATTTGGGTCCTTTTGAGT 1222	
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LOCUS			1222 bp	DNA linear PAT 25-JAN-2001
DEFINITION			Sequence 1 from Patent WO0102578.	
ACCESSION			AX068093	
VERSION			AX068093.1	GI:12578311
KEYWORDS				
SOURCE			Bacillus sp.	
ORGANISM			Bacillus sp.	
REFERENCE			Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.	
AUTHORS			Lian-Hui.Z., Yihu.D. and Jinling.X.	
TITLE			Global regulators of bacterial pathogenic genes: bacterial autoinducer-inactivation protein, as targets for engineering disease resistance	
JOURNAL			Patent: WO 0102578-A 1 11-JAN-2001;	
FEATURES			Institute of Molecular Agrobiolology (SG)	
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Db	359	AAGGACATTTGCGAAGGACAGATTTTACCGAAATGACTGAAGAAGATAGAAATATAG	418
Qy	302	ATATTTTAAACCGGTTGTTATGAGCGCGAAGACCTTCTTTATATTTAGTCTCTCACT	361
Db	419	CTATTTTAAACCGTGGGGGTATGAGCCAGTACCTCTCTATATTTAGTTCACATT	478
Qy	362	TGCATTTTGATCATGACGAGGAATGCGCGTTTATAAATACACCAATCATTTGTACAGC	421
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Qy	422	GTGCTGAATATGAGCGCGCAGATAGCGAAGAAATTTGAAAGAGTGATATCTGCCGA	481
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Qy	482	ATTTAAACTACAAAATCATTTGAAGTGATTTAGAGTCTGTACAGGAGTTCATTTATTCG	541
Db	599	ATTTGAACTACAAAATTTTGAAGGGGATTTGAAGTGGTACCAGGTGTCAACTATTTGT	658
Qy	542	ATACACGAGGCATCTCCAGGCAATCAATCGCTATTTAATTTGAGACAGAAAAATCGGTC	601
Db	659	ATACACGAGGCATTTACACGAGGCATCACTACTATTTAATTTGAGACAGAAAAATCTGGTG	718
Db	1319	CTCATTGGATCCCTTTGAGT	1339
RESULT 4			
AX391415			
LOCUS			
DEFINITION			
Sequence 2 from Patent WO0216623.			
ACCESSION			
AX391415			
VERSION			
AX391415.1			
KEYWORDS			
GI:19700038			
SOURCE			
ORGANISM			
Bacillus thuringiensis			
Bacillus thuringiensis			
Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus; Bacillus			
cereus group.			
REFERENCE			
1			
Zhang, L., Dong, Y. L. and Xu, J.			
Bacterial strains, genes and enzymes for control of bacterial			
diseases by quenching quorum-sensing signals			
Patent: WO 0216623-A 2 28-FEB-2002;			
Institute of Molecular Agrobiolology (SG)			
FEATURES			
Location/Qualifiers			
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/db_xref="taxon:1428"			
/note="Cot1"			
166..918			
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/note="Coding sequence"			
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Query Match			
84.9%; Score 1037; DB 6; Length 1339;			
Best Local Similarity			
90.6%; Pred. No. 2.5e-179;			
Matches 1106; Conservative			
0; Mismatches 115; Indels 0; Gaps 0;			
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Db	119	TTTACTGTATTTACTTTTATCCAAACTAAATGTAAGTGGATACATATGACAGTAAGA	178
Qy	62	AGCTTTATTTGCTCCAGCAGTCTGTTGTATGTTGGATCATCTCTGTTAATAGTACAT	121
Db	179	AGCTTTATTTGCTTCCAGCAGTCTGTTGTATGTTAGATCATCTCTGTTAATAGTACAA	238
Qy	122	TAAACACGAGGAATATTAGACTTACCGGTTTGGTGTATCTTTTGAGACTGAGGAAG	181
Db	239	TCGCGCGGGAATTTATGAACTTACCTGTATGGTGTATCTTTTGAGAGCGGAAGAAG	298
Qy	182	GACCTATTTTAGTAGATACAGGATGCGCAAGAGTGAAGTGAATTAATGAAAGTCTTTTA	241
Db	299	GTCCATTTTAGTAGATACAGGATGCGCAAGAGTGGGTTAATGAAACTTTGTTG	358
Qy	242	ACGGTACATTTGTCGAGGCGAGGTTTACCGAAATGACTGAAGAAGATAGAAATCGTGA	301
Db	359	AAGGACATTTGCGAAGGACAGATTTTACCGAAATGACTGAAGAAGATAGAAATAG	418
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ACCESSION AB017009 AB016877
VERSION AB017009.1 GI:29897026
KEYWORDS Bacillus cereus ATCC 14579
SOURCE Bacillus cereus ATCC 14579
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.
REFERENCE 1 (bases 1 to 301665)
AUTHORS Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B., Kapatal,V., Bhattacharya,A., Reznik,G., Mikhailova,N., Lapidus,A., Chu,L., Mazur,M., Goitsman,E., Larsen,N., D'Souza,M., Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M., Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
TITLE Genome sequence of Bacillus cereus and comparative analysis with Bacillus anthracis
JOURNAL Nature 423 (6935), 87-91 (2003)
MEDLINE 22608415
PUBMED 12721630
REFERENCE 2 (bases 1 to 301665)
AUTHORS Candelon,B., Galloux,K., Ehrlich,D.S. and Sorokin,A.
TITLE The number of ribosomal RNA operons in Bacillus cereus
JOURNAL Unpublished
REFERENCE 3 (bases 1 to 301665)
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AUTHORS

Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B., Kapatal,V., Bhattacharya,A., Reznik,G., Mikhailova,N., Lapidus,A., Chu,L., Mazur,M., Goitsman,E., Larsen,N., D'Souza,M., Walunas,T., Grechkin,Y., Pusch,G., Haselkorn,R., Fonstein,M., Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.
Direct Submission
Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France
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TITLE
JOURNAL

Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France

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source

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AF397400 753 bp DNA linear BCT 24-JUN-2002

LOCUS Bacillus sp. A24 AliiA (aliiA) gene, complete cds.

DEFINITION AF397400

ACCESSION AF397400.1 GI:21541342

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

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FEATURES

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Db 61 GTTAAATAGTACATTAACACAGGAGAAATATTAGACTTACCGGTTTCGGTGTATCTTTG 120

Qy 169 GAGACTGAAGAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAAAT 228

Db 121 GAGACTGAAGAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTGCAGTTAAAT 180

Qy 229 GAAGGTCCTTTTAAACGGTACATTTTTCGAAGGGCAGGTTTTCACGAAATGACTGAAGAA 288

Db 181 GAAGGTCCTTTTAAACGGTACATTTTTCGAAGGGCAGGTTTTCACGAAATGACTGAAGAA 240

Qy 289 GATAGAATCGTGAATATTTTAAACGGTGTGTTTATGAGCGGAGAACCTTCTTTTATTT 348

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Qy 349 ATTAGTTCTCACTTGCATTTTATGATCATGACGAGGAAATGCGCTTTTATAAATACACCA 408

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Qy 649 AATGAAGTCCATTTGCGGATTTGATTCAGAAATAGCTTTTATTCCTCAATTAACGTTTA 708

Db 601 GAGGAAGTCCGCTTTCGTGATTTGATCCAGAAATAGCTTTTATTCCTCAATTAACGTTTA 660

Qy 709 AAGAAGTGGTATCAAAAGAGAGCCGATTTTCTTTGGACATGATATAGAGCAGAA 768

Db 661 AAGAAGTGGTATCAAAAGAGAGCCGATTTTCTTTGGCATGATATAGAGCAGAA 720

Qy 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801

Db 721 AAGGGATGTAAGTGTTCCTCGAATATATATAG 753

RESULT 9

AF478058 753 bp DNA linear BCT 05-AUG-2002

LOCUS Bacillus thuringiensis serovar toumanoffi AliiA-like protein (aliiA)

DEFINITION AF478058

ACCESSION AF478058

VERSION AF478058.1 GI:22095300

KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
PUBMED
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 753)
Lee, S.-Y., Park, S.-Y., Lee, J.-J., Yum, D.-Y., Koo, B.-T. and Lee, J.-K.
Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
Widespread in Many Subspecies of *Bacillus thuringiensis*
Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)
12147491

2 (bases 1 to 753)
Lee, S.-Y., Park, S.-Y., Yum, D.-Y. and Lee, J.-K.
Direct Submission
Submitted (30-JAN-2002) R&D Center, inBionet Corporation,
Jommin-dong 461-6, Yusong, Deajeon 305-390, Korea
Location/Qualifiers

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ORIGIN

Query Match 56.3%; Score 687.4; DB 1; Length 753;
Best Local Similarity 94.6%; Pred. No. 1.5e-115;
Matches 712; Conservative 0; Mismatches 41; Indels 0; Gaps 0;

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1 ATGACAGTAAGAAGCTTTATTCGTCGCCAGCGTGTGTATGTTGGATCAATCGTCT 60

109 GTTATAGTACATTAAACACGAGGAGATTATAGACTACCGTTTGGTGTATCTTTTG 168
61 GTTAACAGTACATTAAACACGAGGAGATTATAGACTACCGTTTGGTGTATCTTTTG 120

169 GAGACTCAAGAAGACCTTTATTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 228
121 GAGACTCAAGAAGACCTTTATTTAGTAGATACAGGTATGCCAGAAAGTCAGTTAATAAT 180

229 GAAGGCTTTTAAACGCTACATTTGTGGAAGGCGAGGTTTACCAGAAATGACTGAAGAA 288
181 GAAGGTTTGTTTAAACGCTACATTTGTGGAAGGCGAGGTTTACCAGAAATGACTGAAGAA 240

289 GATAGATCGTGATATTTTAAACGCGTGTGTATGAGCGGGAAGACCTTCTTTATTT 348
241 GATAGATCGTGATATTTTAAACGCGTGTGTATGAGCGGGAAGACCTTCTTTATTT 300

349 ATTAGTTCTCATTGCTATTTTATGATCATGAGGAGAAATGCGCTTTTATAATACACCA 408
301 ATTAGTTCTCATTGCTATTTTATGATCATGAGGAGAAATGCGCTTTTATAATACACCA 360

409 ATCATTGTACAGCGTGTGTAATATGAGCGGCGGCGAGCATGCGGAAGAAATTTGAAAGAA 468
361 ATCATTGTACAGCGTGTGTAATATGAGCGGCGGCGACCAATAGTAGAATATATGAAGAA 420

QY 469 TGTATATTGCCGAATTTAAACTACAAAATCAATTGAAGGTGATTATGAAGTCGTACCAGAA 528
Db 421 TGTAAATTTGCCCAATTTAAACTACAAAATCAATTGAAGGTGATTATGAAGTCGTACCAGAA 480

QY 529 GTTCAATTTATTCATACACACGAGGCATACCTCAGGGCATCAATCGCTATTATTAATTGAGACA 588
Db 481 GTTCAATTTATTTGTATACACACGAGGCATACCTCAGGGCATCAATCGCTATTATTAATTGAGACA 540

QY 589 GAAAAATCCGCTCTGTATTATTAAAGATTGATGCATCGTATACGAAAGAGAATTTTGAA 648
Db 541 GAGAACTCTGTCAGTGTATTAAACATCGATGATCATGATACAAAAGAAAATTTTGAA 600

QY 649 AATGAAGTCCATTTGGCGGATTTGATTGAGAAATTTAGCTTTTCTCAATTTAAACGTTTA 708
Db 601 GATGAAGTCCATTTGGCGGATTTGATCCAGAAATTTAGCTTTTCTCAATTTAAACGTTTA 660

QY 709 AAAGAAGTGTGATGAAAGAGAGCCGATTTTCTTTTGGACATGATATAGACAGGAA 768
Db 661 AAAGAAGTGTGATGAAAGAGAGCCGATTTTCTTTTGGCGCATGATATAGACAGGAA 720

QY 769 AGGGGATGTAAGTGTTCCTCGAATATATATAG 801
Db 721 AAGGGATGTAAGTGTTCCTCGAATATATATAG 753

RESULT 10
BAC505742 753 bp DNA linear BCT 08-AUG-2003
LOCUS
DEFINITION
Uncultured *Bacillus* sp. aii2 gene for N-acylhomoserine lactone
lactonase.

ACCESSION
VERSION
AJ505742.1 GI:22293638
KEYWORDS
aii2 gene; N-acylhomoserine lactone lactonase.
SOURCE
uncultured *Bacillus* sp.
ORGANISM
uncultured *Bacillus* sp.
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;
environmental samples.

REFERENCE
1
AUTHORS
Carlier, A., Uroz, S., Smadja, B., Fray, R., Latour, X., Dessaux, Y. and
Faure, D.
TITLE
The π Plasmid of *Agrobacterium tumefaciens* Harbors an
atm-Paralogous Gene, aiiB, Also Encoding N-Acyl Homoserine
Lactonase Activity
Appl. Environ. Microbiol. 69 (8), 4989-4993 (2003)

JOURNAL
MEDLINE
22783888
PUBMED
12902298
REFERENCE
2 (bases 1 to 753)
AUTHORS
Fray, R.G.
TITLE
Direct Submission
JOURNAL
Submitted (12-AUG-2002) Fray R.G., School of Biosciences,
University of Nottingham, Sutton Bonington Campus, Loughborough,
Leicestershire, LE12 5LE, UNITED KINGDOM

FEATURES
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ORIGIN	Query Match	55.5%; Score 677.8; DB 1; Length 753;
	Best Local Similarity 93.8%; Pred. No. 8.6e-114;	
	Matches 706; Conservative 0; Mismatches 47; Indels 0; Gaps 0;	
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DB	1 ATGACAGTAAAGAGCTTTATTTTCGCCACGAGGTCGTTGTATGTTGGATCATTCGCTCT 60	
QY	109 GTTAAATAGTACATTAACACGAGGAGATTAATTAGACTTACCGGTTTCGGTGTTATCTTTTG 168	
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DB	61 GTTAAACAGTACATTAACACGAGGGAATTTATAGACTTACCGGTTTCGGTGTTATCTTTTG 120	
QY	169 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCGAGATTAAATAAT 228	
DB		
DB	121 GAGACTGAAGAAGACCTATTTTAGTAGATACAGGTATGCCAGAAAGTCGCGTTAAATAAT 180	
QY	229 GAAGGCTCTTTTAAACGGGTACATTTGTCCGAGGGCAGGTTTTCACGAAAATGACTGAAGAA 288	
DB		
DB	181 GAAGGCCCTTTTAAACGGGTACATTTGTTGAAGGACATATTTTACCAAAAATGACTGAAGAA 240	
QY	289 GATAGAAATCGTGAATATTTTAAAAACGGGTGTTTATGACGCGGAAGACCTTCTTTTATTT 348	
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QY	349 ATTAGTCTTCACCTTGCACTTTTGATCAGTCAGGAGGAAATGCGCTTTTATAAATACACCA 408	
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QY	409 ATCAATTCTACAGCGTGTGAATATGATGAGCGCGCAGCATACGCAAGAAATATTTGAAAGAA 468	
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DB	361 ATTTATTGTGAGCGTGTGAATACGAGCGCGCAACACATGTGAAGAAATATGAAAGAA 420	
QY	469 TGTATATTGCGGAATTTAAACTTACAAATTCATTTGAAGTGATTTATGAAGTCGTACCAGGA 528	
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DB	421 TGTATATTGCGGAATTTGAAATACAAATTCATTTGAAGGGGATTTATGAAGTCGTACCAGGA 480	
QY	529 GTTCCAAATTTATGATACACAGGCGCATCTCCAGGGCATCAATCGCTATTAAATGAGACA 588	
DB		
DB	481 GTTCCAAATTTATGATACACCGAGCATCTACTCCGGGCGATCAGTCGCTATTAAATGAGACA 540	
QY	589 GAAAAATCCCGTCCCTGTATTATTAAACGAATTCATCGTATACGAAAGAGAAATTTTGAA 648	
DB		
DB	541 GAAAAATCCCGTCCCTGTATTATTAAACGAATTCATCGTATACGAAAGAGAAATTTTGAA 600	
QY	649 AATGAAGTGCCATTTGCGGGATTTGAATTCAGAAATAGCTTTATCTTCAATTAAGAGCTTTA 708	
DB		
DB	601 GATGAAGTGCCGCTTCGCTGGAATTTGAATTCGGAATTTAGCTTTATCTTCAATTAAGAGCTTTA 660	
QY	709 AAAGAAGTGTGATCAAAAGAGAGCGGATTTGTTTCTTTGGACATCATATACAGCAGGAA 768	
DB		
DB	661 AAAGAAGTGTGATCAAAAGAGAGAGCCAAATTTGTTTCTTTGGACATCATATACAGCAGGAA 720	
QY	769 AGGGGATGTAAAGTGTTCCTCGAATATATATAG 801	
DB		
DB	721 AAGACTGTGTAAAGTGTTCCTCGAATATATATAG 753	

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481 GTTCGTTATTGTATACACGAGCATTTCTCCAGGCGATCAGTCATTTAATTAGAGACG 540
Db

589 GAAAAATCCGTCCTGTATTATTAAACGATTGATCGATCGTATACGAAAGAGAAATTTTCAA 648
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Db

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Db

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Qy

661 AAAGAAGTGTGATGAAAGAGAACCGGATTTGTTTCTTTGGACATGATATAGACAGAA 720
Db

769 AGGGATGTAAAGTGTTCCTCGAATATATAG 801
Qy

721 AAGGATGTAAAGTGTTCCTCGAATATATAG 753
Db

RESULT 12
AX391419
LOCUS AX391419 753 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 6 from Patent WO0216623.
ACCESSION AX391419
VERSION AX391419.1 GI:19700042
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1
REFERENCE
AUTHORS Zhang,L.; Dong,Y.L. and Xu,J.
TITLE Bacterial strains, genes and enzymes for control of bacterial
diseases by quenching quorum-sensing signals
JOURNAL Patent: WO 0216623-A 6 28-FEB-2002;
Institute of Molecular Agrobiolgy (SG)
FEATURES
source
1. .753
/organism="Bacillus thuringiensis"
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Query Match 52.7%; Score 644.2; DB 6; Length 753;
Best Local Similarity 91.0%; Pred. No. 1.2e-107;
Matches 685; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 49 ATGACAGTAAAGAGCTTTATTTCGTCACGAGTGTGTTGATCTTGGATCATTCGTCT 108
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Qy 109 GTTAAATAGTACATTAACACGAGGAGAAATTAATAGACTTACCGGTTTGGTGTATCTTTTG 168
Db 61 GTTAACTGCTTTAAACACGCGGAAACTATTAACCTTCGCGTTTGGTGTATCTTTTG 120
Qy 169 GAGACTGAAGAGGACCTATTTTAGTAGATACAGTATGCCAGAAAGTCAGTTAATAAT 228
Db 121 CAGACGGAAGAGGTCCTATTATTAGTACACAGGTATGCCAGAAAGTCAGTTAATAAT 180
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Db 181 GAAGGCTTTTAAAGGTACATTTTGAAGAGGACAGATTTTACCGAAATGACGTAGAGAA 240
Qy 289 GATGAATCGTGAAATTTTAAACGGGTGCTTTATGAGCGGAGACCTCTTTTATATT 348
Db 241 GATGAATTTGAATTTTAAACGTCGAGGTATGAGCCAGATGATCTCTTATATT 300
Qy 349 ATTAGTCTCACTGCAATTTTATGATCATGACGAGGAAATGCGGCTTTTATAAATACACCA 408
Db 301 ATTAGTTCGCACTTGCATTTTATGATCATGACGAGGAAATGCGTCTTTTGAATAGGCCA 360

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Qy 409 ATCATTGTACAGCTGCTGAATATATGAGCGGCGAGCATAGCGGAAGAATATTTTGAAGAA 468
Db

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Db

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Db

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Db

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Qy

709 AAAGAAGTGTGATGAAAGAGAACCGGATTTGTTTCTTTGGACATGATATAGACAGAA 768
Db

661 AAAGAAGTGTGATGAAAGAGAACCGGATTTGTTTCTTTGGACATGATATAGACAGAA 720
Qy

769 AGGGATGTAAAGTGTTCCTCGAATATATAG 801
Db

721 AAGGATGTAAAGTGTTCCTCGAATATATAG 753

RESULT 13
AF478052
LOCUS AF478052 753 bp DNA linear BCT 05-AUG-2002
DEFINITION Bacillus thuringiensis serovar kyushuensis AiiA-like protein (aiaA)
gene, complete cds.
ACCESSION AF478052
VERSION AF478052.1 GI:22095288
KEYWORDS
SOURCE
ORGANISM
Bacillus thuringiensis serovar kyushuensis
Bacillus thuringiensis serovar kyushuensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 753)
Lee,S.-J., Park,S.-Y., Lee,J.J., Yum,D.-Y., Koo,B.T. and Lee,J.K.
Genes Encoding the N-Acyl Homoserine Lactone-Degrading Enzyme Are
Widespread in Many Subspecies of Bacillus thuringiensis
Appl. Environ. Microbiol. 68 (8), 3919-3924 (2002)
12147491
2 (bases 1 to 753)
Lee,S.-J., Park,S.-Y., Yum,D.-Y. and Lee,J.-K.
Direct Submission
Submitted (30-JAN-2002) R&D Center, inBionET Corporation,
Jonmin-dong 461-6, Yusong, Deajeon 305-390, Korea
FEATURES
Location/Qualifiers
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ORIGIN	
Query Match	51.9%; Score 634.2; DB 1; Length 753;
Best Local Similarity	90.0%; Pred. No. 7.7e-106;
Matches 678; Conservative	1; Mismatches 74; Indels 0; Gaps 0;
QY	49 ATGACAGTAAAGAGCTTTATTCGTCGCCAGCAGTCTGTGTATGTTGGATCATTCCTCT 108
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QY	109 GTTAATAGTACATTAAACAGAGAGATTAATAGACTTACCGTTTCGTTGTTATCTTTG 168
Db	61 GTTAATAGTACCGTACACCGGGGAATTTATTAACCTTACAGTATCGTGTATTTATG 120
QY	169 GAGACTGAAGAGGACCTATTATTTAGTAGATACAGGTATGCCAGAAAGTGAGTTAAUAT 228
Db	121 GAGACAGAGAGGGCCAAATTTAGTAGATACAGGTATGCCAGAAAGTGCGTTAAUAT 180
QY	229 GAAGGCTCTTTTAAACGGTACATTTGTCGAAGGCGAGGTTTACCGAAAATGACTGAAGAA 288
Db	181 GAAAAATTTATTCGCGTACATTTGTTGAAGGGCAGATTTTACCGAAAATGACTGAAGAA 240
QY	289 GATAGATCGTGAATATTTTAAACGGTGTGTTATGAGCGGAGACCTTCCTTTATTT 348
Db	241 GATAGATCGTGAATATTTTAAAGCGTGTAGGGTATGAGCGGACGACCTTTTATATT 300
QY	349 ATTAGTCTCTACTTGCAATTTTGAATCATGACAGAGAAATGCGCTTTTATTAATACACA 408
Db	301 ATTAGTCTCTACTTGCAATTTTGAACCTATTAATAAATTTTGAAGGGGATTTATGAAGTGTGTTACCGG 360
QY	409 ATCAATGTACAGCGTGTGAATATGAGCGCGGCGAGCATACGGAAGAAATATTGGAAGAA 468
Db	361 ATTCTTGTGACGCGTGTGAATATGAGCGGCACAAATAGTAGAAGAAATATTGAAAGAA 420
QY	469 TGTATATTGCCGAATTTAAACCTACAAATCATGAGTGATTTAGTGTGTCACCGGA 528
Db	421 TGTATATTGCCGAATTTAAACCTACAAATCATGAGGGGAATTTAGAGTGTGTCACCGG 480
QY	529 GTTCAATTTATGTCATACACGAGGCAVATCTCAGGGCATCAATCGCTATTATTAATGAGACA 588
Db	481 GTTCAATTTATGTCATACACGAGGCAVATACACGAGCATCACTATTCAATGAGACG 540
QY	589 GAAAAATCCGTCCTGTATTTAATCAAGTTCATGATCGTATACGAAAGAAATTTGAA 648
Db	541 GAAAACTCTGCCCCAGTGTATTAAACGATCGATCGTATACGAAAGAAATTTTGA 600
QY	649 AATGAGTGCCATTTGCGGGATTGATTCAGAAATGAGCTTTATCTTCAATTAAGGTTTA 708
Db	601 GATGAAGTGGCTTCGCGAGGGTTGATTCGGAATTAGCTTTATCTTCAATTAAGGTTTA 660
QY	709 AAAGAAGTGGTGATGAAGAGAGCCGATTTGTTTCTTTGGACATGATATAGACAGGAA 768
Db	661 AAAGAAATGTTAGAAAGAGAACCCATTTGTTTCTTTGACATGATATAGACAGGAA 720
QY	769 AGGGATGATAAGTGTTCCTTGAATATATATAG 801
Db	721 AAGAGCTGTAAGTGTTCCTTGAATATATATAG 753

RESULT 14
AF350930
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM

753 bp DNA linear BCT 28-MAR-2002
Bacillus thuringiensis AHL-lactonase (aiaA-B17) gene, complete cds.
AF350930
AF350930.1 GI:19773598
Bacillus thuringiensis
Bacillus thuringiensis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL
FEATURES

1 (bases 1 to 753)
Dong Y.H., Gusti,A.R., Zhang, Q., Xu,J.L. and Zhang,L.H.
Identification of quorum-quenching N-acyl homoserine lactonases
from Bacillus species
Appl. Environ. Microbiol. 68 (4), 1754-1759 (2002)
21914084
11916693
2 (bases 1 to 753)
Dong,Y.H., Gusti,A., Xu,J.L. and Zhang,L.H.
Direct Submission
Submitted (21-FEB-2001) Institute of Molecular Agrobiolgy, The
National University of Singapore, 1 Research Link, Singapore 117604
Location/Qualifiers

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gene
CDS

ORIGIN

Query Match	51.8%; Score 633.6; DB 1; Length 753;
Best Local Similarity	90.2%; Pred. No. 9.9e-106;
Matches 678; Conservative	0; Mismatches 74; Indels 0; Gaps 0;
QY	49 ATGACAGTAAAGAGCTTTATTCGTCGCCAGCAGTCTGTGTATGTTGGATCATTCCTCT 108
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QY	109 GTTAATAGTACATTAAACAGAGAGATTTATAGACTTACCGTTTCGTTGTTATCTTTG 168
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QY	169 GAGACTGAAGAGGACCTATTATTTAGTAGATACAGGTATGCCAGAAAGTGCGAGTTAAUAT 228
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QY	289 GATAGATCGTGAATATTTTAAACGGTGTGTTATGAGCGGCGAGGACCTTCCTTTATATT 348
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QY	349 ATTAGTCTCTACTTGCAATTTTGAATCATGACAGAGAAATGCGCTTTTATTAATACACA 408
Db	301 ATTAGTCTCTACTTGCAATTTTGAACCTATTAATAAATTTTGAAGGGGATTTATGAAGTGTGTTACCGG 360
QY	409 ATCAATGTACAGCGTGTGAATATGAGCGCGGCGAGCATACGGAAGAAATATTGGAAGAA 468
Db	361 ATTCTTGTGACGCGTGTGAATATGAGCGGCACAAATAGTAGAAGAAATATTGAAAGAA 420
QY	469 TGTATATTGCCGAATTTTAAACCTACAAATCATTTGAAGTGTATTTGAAGTGTGTTACCGGA 528
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QY	529 GTTCAATTTATGTCATACACGAGGCAVATCTCAGGGCATCAATCGCTATTATTAATGAGACA 588

Db	481	GTTCATATTGTATACGCCAGGTCATCTCTCCAGGCCATCAGTCGCTATTATTAGACA	540
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LOCUS	AX391418	753 bp	DNA linear PAT 23-MAR-2002
DEFINITION	Sequence 5 from Patent WO0216623.		
ACCESSION	AX391418		
VERSION	AX391418.1 GI:19700041		
KEYWORDS	Bacillus thuringiensis		
SOURCE	Bacillus thuringiensis		
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.		
REFERENCE	1		
AUTHORS	Zhang, L., Dong, Y. l. and Xu, J.		
TITLE	Bacterial strains, genes and enzymes for control of bacterial diseases by quenching quorum-sensing signals		
JOURNAL	Patent: WO 0216623-A 5 28-FEB-2002;		
	Institute of Molecular Agrobiolology (SG)		
FEATURES	Location/Qualifiers		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:1428"		
	/note="B17"		
ORIGIN			
Query Match 51.8%; Score 633.6; DB 6; Length 753;			
Best Local Similarity 90.2%; Pred. No. 9.9e-106;			
Matches 678; Conservative 0; Mismatches 74; Indels 0; Gaps 0;			
Qy	49	ATGACAGTAAAGAACCTTTATTTCTGCCAGCAGTCTGTGTATGTTGATCGATCATTCGTCT	108
Db	1	ATGACAGTAAAGAACCTTTATTTCTGCCAGCAGTCTGTGTATGTTGATCGATCATTCGTCT	60
Qy	109	GTTAATAGTACATTAAACACAGGAGAAATTTAGACTTTACCGTTCGGTGTATCTTTTG	168
Db	61	GTTAATAGTACACTCGCGCCGGGAATTTATTGAACCTTACCTGTATGGTGTATCTTTTG	120
Qy	169	GAGACTGAAGAGGACCTATTTTAGTAGATACAGTATGCCAGAAAGTGCAGTTAAATAT	228
Db	121	GAGACAGAAGAGGGCCCTATTTTAGTAGATACAGTATGCCAGAAAGTGCAGTTAAATAT	180
Qy	229	GAAGGTCTTTTAAACGGTACATTTCTGCAAGGGCAGGTTTACCGAAAATGACTGAAGAA	288
Db	181	GAAGGGCTTTTAAACGGTACATTTCTGCAAGGACAGATTTTACCGAAAATGACTGAAGAA	240
Qy	289	GATAGAATCGTGAATATTTTAAACGGGTGGTTATGAGCGGGAAGACCTTCTTTATATT	348
Db	241	GATAGAATCGTGAATATATAAAGCGTGTAGGATGAGCGGACGACCTTTTATATATT	300
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Db	301	ATTAGTCTCTACTTTGATCATGAGAGGAAACGGTGTCTTTTACAAATACACCG	360
Qy	409	ATCATTTGTACAGCGTGCTGAATATGAGCGCGCAGCATAGCGAAGAAATTTTGAAGAA	468

Db	361	ATTATTGTGCAACGAATATGAGCAGCACCTTCTATAGAGAGATATATGAAAGAA	420
Qy	469	TGTATATTGCCGAATTTAAACTACAAATCAATTGAAGTGATTTATGAAGTCGTACCCAGGA	528
Db	421	TGTATATTACCGCATTTGAACTATAAAATTTATGAAAGGGGATTTATGAAGTGTACCAAGT	480
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Qy	589	GAAGAAATCCGGTCTCTGTATTATTAAACGATTGATCGATCGTATACGAAGAGAAATTTTGAA	648
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Db	661	AAAGAAGTTGTGATGAAGAGAGAGCCAAATTTTCTTTGGTCAIGATATAGAACAGGAA	720
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Search completed: February 24, 2004, 03:41:00
Job time : 3433 secs

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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:19:22 ; Search time 17 Seconds
(without alignments)
691.569 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTKKLYFPVAGRCMLDHSS.....VFFGHDIQERGCKVFPFYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	11.9	310	1 YN00_MYCTU	Q50665 mycobacteri
2	152	11.6	203	1 Y296_METJA	Q57744 methanococc
3	135	10.3	264	1 YFLN_BACSU	Q34409 bacillus su
4	116	8.8	211	1 Y135_AQUAE	Q67893 aquifex aeo
5	115.5	8.8	428	1 Y047_METJA	Q60355 methanococc
6	114.5	8.7	331	1 GL2M_ARATH	Q24495 arabidopsi
7	113	8.6	206	1 Y888_METJA	Q58298 methanococc
8	112.5	8.6	212	1 YCBL_HAEIN	Q57544 haemophilus
9	110.5	8.4	290	1 BLA1_XANMA	P52700 xanthomonas
10	109.5	8.3	274	1 GLO2_YEAST	Q05584 saccharomyc
11	107	8.1	211	1 YQGX_BACSU	P34501 bacillus su
12	106.5	8.1	215	1 YCBL_ECOLI	P55849 escherichia
13	105.5	8.0	281	1 YND2_YEAST	P53965 saccharomyc
14	100.5	7.6	258	1 GL2C_ARATH	Q24496 arabidopsi
15	99.5	7.6	220	1 YVBB_BACSU	P37502 bacillus su
16	96	7.3	474	1 C1SY_EMENI	Q00098 emericella
17	96	7.3	610	1 GIDA_CHLMU	Q9pjp3 chlamydia m
18	95.5	7.3	479	1 C1SY_YEAST	P00890 saccharomyc
19	94.5	7.2	319	1 YQJP_BACSU	P54553 bacillus su
20	94.5	7.2	543	1 Y274_METJA	Q57722 methanococc
21	94	7.1	475	1 C1SY_ASPNG	P51044 aspergillus
22	93.5	7.1	250	1 GLO2_BUCAP	Q08889 buchnera ap
23	92	7.0	1609	1 YL54_CAEEL	P34434 caenorhabdi
24	91	6.9	260	1 GLO2_HUMAN	Q16775 homo sapien
25	90.5	6.9	706	1 PKSL_DROME	Q24323 drosophila
26	90.5	6.9	4427	1 YKSL_BACSU	Q05470 bacillus su
27	90	6.8	251	1 GLO2_BUCAI	P57336 buchnera ap
28	89	6.8	254	1 BLAB_AERYH	P26918 aeromonas h
29	89	6.8	294	1 Y301_METJA	P77749 methanococc
30	89	6.8	1018	1 FNBA_STAAU	P14738 staphylococ
31	88.5	6.7	260	1 GLO2_CALJA	Q28333 callithrix
32	87.5	6.7	383	1 DGT1_RICPR	Q9ze82 rickettsia
33	87.5	6.7	421	1 Y162_METJA	Q57626 methanococc

34	87	6.6	448	1 Y861_METJA	Q58271 methanococc
35	86.5	6.6	256	1 Y448_METJA	Q57890 methanococc
36	86.5	6.6	285	1 GLO4_YEAST	Q12320 saccharomyc
37	86.5	6.6	1104	1 BUD2_YEAST	P33314 saccharomyc
38	86.5	6.6	1181	1 ITA2_HUMAN	P17301 homo sapien
39	86	6.5	371	1 CARA_PYRFU	Q80086 pyrococcus
40	86	6.5	404	1 FPR4_METTM	Q50497 methanobact
41	85.5	6.5	434	1 ENO_STAEP	Q8cpj3 staphylococ
42	85.5	6.5	449	1 TL40_SPIOL	Q49939 spinacia ol
43	85	6.5	356	1 YXT2_CAEEL	Q18078 caenorhabdi
44	85	6.5	612	1 MCR_XENLA	Q91573 xenopus lae
45	85	6.5	637	1 GYRE_TREPA	O08399 treponema p

ALIGNMENTS

RESULT 1					
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ID	YN00_MYCTU	STANDARD;	PRT;	310 AA.	
AC	Q50665;				
DT	01-NOV-1997 (Rel. 35, Created)				
DT	01-NOV-1997 (Rel. 35, Last sequence update)				
DT	28-FEB-2003 (Rel. 41, Last annotation update)				
DE	Hypothetical protein Rv2300c.				
GN	Rv2300C OR MT2357 OR MTCY339.09.				
OS	Mycobacterium tuberculosis.				
OC	Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;				
OC	Corynebacterineae; Mycobacteriaceae; Mycobacterium.				
OX	NCBI_TaxID=1773;				
RN	[1]				
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RC	STRAIN=H37RV;				
RX	MEDLINE=98295987; PubMed=9634230;				
RA	Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,				
RA	Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,				
RA	Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,				
RA	Davies K., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,				
RA	Hornsey T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,				
RA	Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,				
RA	Rutter S., Seeger K., Skelton S., Squares S., Squares R.,				
RA	Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;				
RT	"Deciphering the biology of Mycobacterium tuberculosis from the				
RT	complete genome sequence."				
RL	Nature 393:537-544(1998).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=CDC 1551 / Oshkosh;				
RA	Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,				
RA	Peterson J., DeBoy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,				
RA	Kolony J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,				
RA	Delcher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,				
RA	Bisshai W.;				
RT	"Whole genome comparison of Mycobacterium tuberculosis clinical and				
RT	laboratory strains."				
RL	Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.				
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CC	-----				
DR	EMBL; Z77163; CAB00971.1; --				
DR	EMBL; AE007078; AK46642.1; --				
DR	PIR; H70733; H70733.				
DR	TIGR; MT2357; --				
DR	TubercuList; Rv2300c; --				
DR	InterPro; IPR001279; Blactmase-like.				
DR	Pfam; PF00753; lactamase_B; l.				
KW	Hypothetical protein; Complete proteome.				

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QY	236	D 236
Db	299	D 299
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DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Hypothetical protein M20296.	
GN	M20296.	
OS	Methanococcus jannaschii.	
OC	Archaea; Euryarchaeota; Methanococci; Methanococcales;	
OC	Methanocaldococcaceae; Methanocaldococcus.	
OX	NCBI_TaxID=2190;	
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RA	Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,	
RA	Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,	
RA	Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,	
RA	Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,	
RA	Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,	
RA	Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,	
RA	Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;	
RT	"Complete genome sequence of the methanogenic archaeon, Methanococcus	
RT	jannaschii".	
RL	Science 273:1058-1073 (1996).	
CC	!- SIMILARITY: WEAK, TO M.JANNASCHII M20888.	
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CC	-----	
DR	EMBL; U67484; AAB98284.1; -	
DR	PIR; A64337; A64337.	
DR	TIGR; M20296; -	
DR	InterPro; IPR001279; Blactmase-like.	
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KW	Hypothetical protein; Complete proteome.	
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Db	44	LIITDNNNIIVDTSTKDM-----ENIIIGLSLNLSPNDID 80	
QY	99	YIISHLHFDHAGNGAFINTPIIVQAEVAAQHSSEYVLEKICILPNLVN 158	
Db	81	VINTLHLDHITENNPIFKNATFYASPKFPGFNDNFDFK-----FK-----DKE-- 126	
QY	159	PGVQLLHTPGHTPGHQSLLIETEKSGPVLITIDASYTKENFENEV-PFAGFDSALSSI 217	
Db	127	-----IEIETGHTVGSISVIYK-----DYVVGSDASPLKNILKMPKLVNDEKLALES 179	
QY	218	KRLKE-----VVMKEK 228	
Db	180	KKIRLKRKNVITGHEGIVYVKEK 201	
RESULT 3			
YFLN_BACSU	ID	YFLN_BACSU	STANDARD; PRT; 264 AA.
AC	O34409;		
DT	28-FEB-2003 (Rel. 41, Created)		
DT	28-FEB-2003 (Rel. 41, Last sequence update)		
DT	28-FEB-2003 (Rel. 41, Last annotation update)		
DE	YflN protein.		
GN	YFLN.		
OS	Bacillus subtilis.		
OC	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.		
OX	NCBI_TaxID=1423;		
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RC	MEDLINE=97417488; PubMed=9272861;		
RA	Yamamoto H., Uchiyama S., Nugroho F.A., Sekiguchi J.;		
RT	"Cloning and sequencing of a 35.7 kb in the 70 degree-73 degree region		
RT	of the Bacillus subtilis genome reveal genes for a new two-component		
RT	system, three spore germination proteins, an iron uptake system and a		
RT	general stress response protein."		
RT	Gene 194:191-199 (1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=168;		
RC	MEDLINE=98044033; PubMed=9384377;		
RA	Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,		
RA	Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,		
RA	Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,		
RA	Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,		
RA	Choi S.K., Codani J.J., Connerton I.F., Cummings N.J., Daniel R.A.,		
RA	Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,		
RA	Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,		
RA	Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,		
RA	Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,		
RA	Guiseppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,		
RA	Hubert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,		
RA	Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,		
RA	Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,		
RA	Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,		
RA	Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,		
RA	Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,		
RA	Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,		
RA	Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,		
RA	Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,		
RA	Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y.,		
RA	Sato T., Scanlan E., Schleich S., Schroeter R., Scofield F.,		
RA	Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,		
RA	Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,		
RA	Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,		
RA	Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,		
RA	Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,		

DE Hypothetical protein MJ0047.
GN MJ0047.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,
RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.,
RA "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii.";
RL Science 273:1058-1073(1996).
CC -I- SIMILARITY: STRONG TO M.JANNASCHII MJ0162 AND MJ1236. ALSO
CC SIMILAR TO SYNECHOCYSTIS PCC 6803 SLL0514.
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CC EMBL; U67462; AAB98027.1; --
CC TIGR; MJ0047; --
CC InterPro; IPR001279; Lactamase-like.
DR Pfam; PF00753; lactamase_B; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 428 AA; 48492 MW; A649ED66705AA01B CRC64;

Query Match 8.8%; Score 115.5; DB 1; Length 428;
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Matches 51; Conservative 44; Mismatches 73; Indels 77; Gaps 10;

Qy 28 GEILDLPWCYLLTEGPIIVDPMPESAVNNEGLFNGFVGQVLPKMTEDRIUNIL 87
Db 7 GAALVGRSGTEIKTKSKILLDCGVK-----LGKEIEYPILDNSI 47

Qy 88 KRVCYEPEDLLYISSLHFDHAGNGAF---INTPLI-----VQR 125
Db 48 RDV-----DKVFI--SHALDHSGLPVLPHRKMVDPVITTELSKKLIKVLKDMVKIAE 100

Qy 126 AEYEAQAQHSBEYLKECI---LP-NLNYKIIIEGDYEVVPGVQLLTPGHTPGHQSLLIETE 181
Db 101 TENKKIPYNNHDVKEARHTIPLNVDNKKYKDFSYE-----LFSAGHIGPSASILLNYQ 155

Qy 182 KSGPVILT-----IDASYKENPENVPFAGFDEL-----ALSIRKLK 221
Db 156 NNKTIILTGVKLRDTRLTGKADLSYTKDDILIIESTYGNISHPDKAVELSPFIEKIK 215

Qy 222 EVNMK 226
Db 216 EILFR 220

RESULT 6
GL2M_ARATH STANDARD; PRT; 331 AA.
AC O24495; O22857; O24494;
DT 15-DEC-1998 (Rel. 37, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hydroxyacylglutathione hydrolase, mitochondrial precursor (EC 3.1.2.6)
DE (Glyoxalase II) (Glx II).

GN GLX2-1 OR AT2G43430 OR TIO24.17
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Wassilewskija;
RX MEDLINE=98009983; PubMed=9349270;
RA Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
RT "Molecular characterization of glyoxalase II from Arabidopsis
RL thaliana.";
RN Plant Mol. Biol. 35:471-481(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umayam L.,
RA Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
RA Venter J.C.;
RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
RL thaliana.";
RN Nature 402:761-768(1999).
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia; R.W., Ecker J.R., Theologis A.;
RX "RIKEN Arabidopsis full length cDNA clones (RAPFs) sequenced by the
RT SRIK consortium (Salk/Stanford/PGEC).";
CC Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -I- FUNCTION: THIOLESTERASE THAT CATALYZES THE HYDROLYSIS OF S-D-
CC LACTOYL-GLUTATHIONE TO FORM GLUTATHIONE AND D-LACTIC ACID.
CC -I- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
CC Glutathione + a 2-hydroxy acid anion.
CC -I- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -I- PATHWAY: Glyoxal pathway.
CC -I- SUBCELLULAR LOCATION: Mitochondrial.
CC -I- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U90927; AAC49865.1; --
CC EMBL; U90928; AAC49866.1; --
CC EMBL; AC002335; AAB64315.2; --
CC EMBL; AY091278; AAM14217.1; --
CC EMBL; AY063806; AAL36162.1; --
CC HSSP; Q16775; 1QH5.
CC InterPro; IPR001279; Lactamase-like.
CC Pfam; PF00753; lactamase_B; 1.
KW Hydrolase; Zinc; Mitochondrion; Transit peptide.
FT TRANSIT 1 76 MITOCHONDRION (POTENTIAL).
FT CHAIN 77 331 HYDROXYACYLGLUTATHIONE HYDROLASE.
FT METAL 131 131 ZINC 1 (BY SIMILARITY).
FT METAL 133 133 ZINC 1 (BY SIMILARITY).
FT METAL 135 135 ZINC 2 (BY SIMILARITY).
FT METAL 136 136 ZINC 2 (BY SIMILARITY).
FT METAL 189 189 ZINC 1 (BY SIMILARITY).
FT METAL 208 208 ZINC 1 AND 2 (BY SIMILARITY).
FT CONFLICT 159 159 D -> H (IN REF. 1; AAC49866).
SQ SEQUENCE 331 AA; 36499 MW; 2EDC21B4902419C5 CRC64;

RESULT 8		
YCBL_HAEIN	STANDARD;	PRT; 212 AA.
ID_YCBL_HAEIN		
AC_Q57544		
DT_01-NOV-1997	(Rel. 35, Created)	
DT_28-FEB-1997	(Rel. 35, last sequence update)	
DT_28-FEB-2003	(Rel. 41, last annotation update)	
DE		

```

OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OC NCBI_TaxID=727;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Rd / KW20 / ATCC 51907;
RC MEDLINE=95350630; PubMed=7542800;
RX Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McClellan K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,
RA Utterback T.R., Hanna M.C., Spriggs T., Saudek D.M., Brandon R.C.,
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae
RT Rd.";
RL Science 269:496-512(1995).
RC -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY. STRONG, TO E.COLI
CC YCBL.
CC
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CC
CC EMBL; U32839; AAC23309.1; -
CC PIR; D64174; D64174.
CC TIGR; H11663; -.
CC
CC InterPro; IPR001279; Blactamase-like.
CC Pfam; PF00753; lactamase_B; 1.
CC
CC Hypothetical protein, Hydrolase; Zinc; Complete proteome.
CC FT METAL 55 55 ZINC 1 (BY SIMILARITY).
CC FT METAL 57 57 ZINC 1 (BY SIMILARITY).
CC FT METAL 59 59 ZINC 2 (BY SIMILARITY).
CC FT METAL 60 60 ZINC 2 (BY SIMILARITY).
CC FT METAL 132 132 ZINC 1 (BY SIMILARITY).
CC FT METAL 151 151 ZINC 1 AND 2 (BY SIMILARITY).
CC FT METAL 152 152 ZINC 2 (BY SIMILARITY).
CC SEQUENCE 212 AA; 23882 MW; 4039D4E7DA445F4AA CRC64;
CC
CC
CC Query Match 8.6%; Score 112.5; DB 1; Length 212;
CC Best Local Similarity 24.6%; Pred No 0.018;

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EMBL; X75074; CAA52968.1; -
PIR; S45349; S45349.
PDB; 1SML; 20-SEP-99.
InterPro; IPR001018; Beta lactamase B.
InterPro; IPR001279; Blactamase-like.
Pfam; PF00753; lactamase B; 1.
PROSITE; PS00743; BETA LACTAMASE B.1; 1.
PROSITE; PS00744; BETA LACTAMASE B.2; FALSE NEG.
KW Hydrolase; Zinc; Antibiotic resistance; Periplasmic; Signal;
3D-structure. 1 21 POTENTIAL.
FT SIGNAL 22 33
FT PROPEP 22 33 METALLO-BETA-LACTAMASE L1.
FT CHAIN 34 290
FT DISULFID 239 267
FT METAL 105 105 ZINC 1.
FT METAL 107 107 ZINC 1.
FT METAL 109 109 ZINC 2.
FT METAL 181 181 ZINC 1.
FT METAL 205 205 ZINC 2.
FT METAL 217 217 ZINC 2.
FT CONFLICT 36 37 AS -> QR (IN REF. 2).
FT CONFLICT 40 40 Q -> A (IN REF. 2).
FT CONFLICT 56 58 TED -> ROH (IN REF. 2).
FT CONFLICT 63 63 L -> H (IN REF. 2).
FT HELIX 36 39
FT STRAND 41 41
FT STRAND 45 48
FT TURN 49 50
FT STRAND 51 53
FT STRAND 56 56
FT TURN 57 58
FT STRAND 59 59
FT STRAND 62 66
FT TURN 67 68
FT STRAND 69 73
FT STRAND 76 76
FT HELIX 78 80
FT HELIX 81 90
FT TURN 91 92
FT HELIX 95 97
FT STRAND 98 102
FT HELIX 108 111
FT TURN 112 113
FT HELIX 114 120
FT STRAND 124 127
FT HELIX 129 136
FT TURN 137 139
FT STRAND 142 142
FT TURN 143 145
FT STRAND 146 146
FT TURN 147 147
FT STRAND 158 159
FT TURN 162 163
FT STRAND 165 168
FT TURN 169 170
FT STRAND 171 177
FT TURN 183 184
FT STRAND 186 194
FT TURN 195 196
FT STRAND 197 203
FT TURN 210 211
FT TURN 218 219
FT TURN 221 222
FT HELIX 223 235
FT TURN 236 236
FT STRAND 241 243
FT HELIX 247 250
FT TURN 251 251

Matches 51; Conservative 29; Mismatches 56; Indels 71; Gaps 11;
QY 79 EEDRIWNILKRYGEPEDLLIYIISHLPHDAGNGAFINTPIIVORAEYEAQH-----133
Db 33 EAERLIQRLELDL---NLKVLTLTHGLDHVG-----AAMQLKQHPGVRI 75
QY 134 -----SEVYKSCI-----LPNLNYKI-----IEGDYEVVPG--VQLLHTPGHTG 172
Db 76 WGSNEKDKLFESLPQAOQFGLPNDIDAFDPWFNQEGEILKLDGFGNFELHLPHTG 135
QY 173 HQSLLETGKSGVLLTIDASYTKENFENEVPAG-----PSELALSSIKRLKEV 223
Db 136 HIG-FIEHEK-----KVAFTGVLFGQIGRTDPRGRGYEYLISII-RTKLL 180
QY 224 VMKEKPIVFVFGH-----DIEQERGCKVF 246
Db 181 PLNDIIIIAGHSGYTTIGQEKRSNPF 207
RESULT 9
BLA1_XANMA STANDARD; PRT; 290 AA.
AC P52700;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Metallo-beta-lactamase L1 precursor (Beta-lactamase, type II)
DE (EC 3.5.2.6) (Penicillinase).
OS Xanthomonas maltophilia (Pseudomonas maltophilia) (Stenotrophomonas maltophilia).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Stenotrophomonas.
OX NCBI_TaxID=40324;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IID 1275.
RX MEDLINE=34289479; PubMed=8018721;
RA Walsh T.R., Hall L., Assinder S.J., Nichols W.W., Cartwright S.J.,
RA Macgowan A.P., Bennett P.M.;
RT "Sequence analysis of the L1 metallo-beta-lactamase from Xanthomonas maltophilia".
RL Biochim. Biophys. Acta 1218:199-201(1994).
RN [2]
RP SEQUENCE OF 34-65.
RC STRAIN=IID 1275;
RX MEDLINE=86025393; PubMed=3931629;
RA Bicknell R., Emanuel E.L., Gagnon J., Waley S.G.;
RT "The production and molecular properties of the zinc beta-lactamase of Pseudomonas maltophilia IID 1275".
RL Biochem. J. 229:791-797(1985).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS).
RX MEDLINE=99030465; PubMed=9811546;
RA Ullah J.H., Walsh T.R., Taylor I.A., Emery D.C., Verma C.S.,
RA Gamblin S.J., Spencer J.;
RT "The crystal structure of the L1 metallo-beta-lactamase from Stenotrophomonas maltophilia at 1.7 A resolution".
RL J. Mol. Biol. 284:125-136(1998).
CC 1- FUNCTION: HAS A HIGH ACTIVITY AGAINST IMPENEM. UNSTABLE BELOW PH 8. UNLESS ZINC IS PRESENT.
CC 1- CATALYTIC ACTIVITY: A beta-lactam + H(2)O = a substituted beta-amino acid.
CC 1- COFACTOR: BINDS TWO ZINC IONS PER MOLECULE.
CC 1- ENZYME REGULATION: Inhibited by Hg(2+) or Cu(2+). Reduced enzymatic activity in presence of Co(2+), Ni(2+), Cd(2+), and Mn(2+).
CC 1- SUBUNIT: Homotetramer.
CC 1- SUBCELLULAR LOCATION: Periplasmic (Potential).
CC 1- SIMILARITY: Belongs to the class-B beta-lactamase family.

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FT HELIX 254 259
 FT TURN 260 263
 FT HELIX 267 287
 SQ SEQUENCE 290 AA; 30801 MW; 0B34CAB5451B8C1E CRC64;

Query Match 8.4%; Score 110.5; DB 1; Length 290;
 Best Local Similarity 21.5%; Pred. No. 0.039;
 Matches 40; Conservative 30; Mismatches 57; Indels 59; Gaps 7;

QY 39 LLETEEGILVDTGMPESAVNNEGLFNGTFVEGVQLPKQWTDREDRIVNLKRVGVEPEDLL 98
 Db 63 LVQPDGVAVLDDGGMPQMA-----SHLLDNMKARGVTPRDLR 99
 QY 99 YIISHLHFDHAGNGAFINPTI--IVQRAEYEAQHSEEVYKGCIL----- 143
 Db 100 LILLSHAHADHAG-----PVALKRRTGAKVAANAE-----SAVLLARGSGDDLHFGD 147
 QY 144 -----PNLNKIIIEGDEYVGVQVLL--HTFGHTPGHQS--LLIETEKSGPVLITIDASY 194
 Db 148 GITYPANADRIVDGEVITVGGIVFTAHFVAGHTPGSTANTWDTTRNGKPVRIAYADSL 207
 QY 195 TKNFPE 200
 Db 208 SAPGYQ 213

RESULT 10
 GLO2_YEAST STANDARD; PRT; 274 AA.
 AC Q05584;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Hydroxyacylglutathione hydrolase, cytoplasmic isozyme (EC 3.1.2.6)
 DE (Glyoxalase II) (Glx II).
 GN GLO2 OR YDR272W OR D9954.5.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=W303;
 RX MEDLINE=97407946; PubMed=9261170;
 RA Bito A., Haider M., Hadler I., Breitenbach M.;
 RT "Identification and phenotypic analysis of two glyoxalase II encoding
 RT genes from Saccharomyces cerevisiae, GLO2 and GLO4, and intracellular
 RT localization of the corresponding proteins.";
 RL J. Biol. Chem. 272:21509-21519(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z.,
 RA Favell A., Fulton L., Gattung S., Greco T., Kirsten J.,
 RA Kucaba T., Hallsworth K., Hawkins J., Hillier L., Jier M.,
 RA Johnson D., Johnson L., Langston Y., Latreille P., Le T.,
 RA Mardis E., Meneses S., Miller N., Nhan M., Pauley A., Peluso D.,
 RA Rifken L., Riles L., Taich A., Trevisan E., Vignati D.,
 RA Wilcox L., Wohldman P., Vaudin M., Wilson R., Waterston R.;
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Thiolesterase that catalyzes the hydrolysis of S-D-
 CC lactoyl-glutathione to form glutathione and D-lactic acid.
 CC -1- CATALYTIC ACTIVITY: (S)-(2-hydroxyacyl)glutathione + H(2)O =
 CC glutathione + a 2-hydroxy acid anion.
 CC -1- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
 CC -1- PATHWAY: Glyoxal pathway.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
 CC -----
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 CC -----
 DR EMBL; Y10292; CAA71335.1; -;
 DR EMBL; U51030; AAB64450.1; -;
 DR PIR; S70130; S70130.
 DR HSSP; Q16775; 1QH5.
 DR SGD; S0002680; GLO2.
 DR GO; GO:0005737; C:cytoplasm; IDA.
 DR GO; GO:0004416; F:hydroxyacylglutathione hydrolase activity; IMP.
 DR GO; GO:0005975; P:carbohydrate metabolism; IMP.
 DR InterPro; IPR001279; Blacktmase-like.
 DR Pfam; PF00753; lactamase B; 1.
 DR Hydroxylase; Zinc; Multigene family.
 FT METAL 59 59 ZINC 1 (BY SIMILARITY).
 FT METAL 61 61 ZINC 1 (BY SIMILARITY).
 FT METAL 63 63 ZINC 2 (BY SIMILARITY).
 FT METAL 64 64 ZINC 2 (BY SIMILARITY).
 FT METAL 121 121 ZINC 1 (BY SIMILARITY).
 FT METAL 144 144 ZINC 1 AND 2 (BY SIMILARITY).
 FT METAL 188 188 ZINC 2 (BY SIMILARITY).
 SQ SEQUENCE 274 AA; 31326 MW; 6CD7AB9F0A9399EA CRC64;

Query Match 8.3%; Score 109.5; DB 1; Length 274;
 Best Local Similarity 21.8%; Pred. No. 0.044;
 Matches 50; Conservative 40; Mismatches 82; Indels 57; Gaps 11;

QY 36 WCYLETEEG--PILVDTGMPESAVNNEGLFNGTFVEGVQLPKQWTDREDRIVNLKRVGYE 93
 Db 17 YCILLSDSKNKSWLIDPAEPP-----EVLPELDEK1----- 50
 QY 94 PEDLLYIISHLHFDHAGNGAFI-----NTPIIQRAEYEAQHSEEVYKGCILPNLNY 148
 Db 51 --SVEAIWTHHHYDHADGNADILKYLKKNP---TSKVEVIGSGKDCPKVTIIPENLK 104
 QY 149 KILEGDEYVGVQVLLHPTGHTPGHQSLLIETEKSGP-VLLITIDASYTK--ENFENEVPP 205
 Db 105 KLHLGDLLEIT---CIRTPCHTRDISICYVYKDPPTTDERCIFTGTLFTAGCGRP---F 155
 QY 206 AGFDSSELALSSIKRLKEVNMKE---KPIVFFGHDIQER---GCKVFPE 248
 Db 156 EGIGEEMDIALNNSILETVGRQNSKTRVTPGHEYTSNVKVRKIYPQ 204

RESULT 11
 YQGX_BACSU STANDARD; PRT; 211 AA.
 ID YQGX_BACSU STANDARD; PRT; 211 AA.
 AC P5450L; 1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein yqgx.
 GN YQGX.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / JH642;
 RX MEDLINE=97124185; PubMed=8969508;
 RA Mizuno M., Masuda S., Takemaru K.-I., Hosono S., Sato T., Takeuchi M.,
 RA Kobayashi Y.;
 RT "Systematic sequencing of the 283 kb 210 degrees-232 degrees region of
 RT the Bacillus subtilis genome containing the skin element and many
 RT sporulation genes.";
 RL Microbiology 142:3103-3111(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
 RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,

RA Borriss R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
 RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
 RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
 RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
 RA Entian K.D., Errington J., Fabret C., Ferrai E., Foulger D.,
 RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
 RA Ghim S.Y., Glaeser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guisepi G., Guy B.J., Haga K., Haeche J., Harwood C.R., Henaut A.,
 RA Hilbert H., Hollappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
 RA Joris B., Karamata D., Kasahara Y., Klaere-Blanchard M., Klein C.,
 RA Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moesti D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
 RA Rieger M., Rivolta C., Rochelle E., Roche B., Rose M., Sadaie Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Serron P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
 RA Tosato V., Uchiyama S., Vandenberg M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.,
 RA "The complete genome sequence of the Gram-positive bacterium Bacillus
 RT subtilis."
 RL Nature 390:249-256(1997).
 CC -1- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
 CC
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 CC
 CC EMBL; D84432; BAA12527.1; --
 CC EMBL; Z99116; CAB14410.1; --
 CC PIR; A69958; A69958.
 CC Subtilisin; BG11691; YggX.
 CC InterPro; IPR001279; Bactamase-like.
 CC Pfam; PF00753; lactamase B; 1.
 CC Hypothetical protein; Hydrolase; Zinc; Complete proteome.
 CC METAL 54 54 ZINC 1 (BY SIMILARITY).
 CC METAL 56 56 ZINC 1 (BY SIMILARITY).
 CC METAL 58 58 ZINC 2 (BY SIMILARITY).
 CC METAL 59 59 ZINC 2 (BY SIMILARITY).
 CC METAL 130 130 ZINC 1 (BY SIMILARITY).
 CC METAL 149 149 ZINC 1 AND 2 (BY SIMILARITY).
 CC METAL 190 190 ZINC 2 (BY SIMILARITY).
 CC SEQUENCE 211 AA; 23225 MW; 1EDA9355F9F8E4F0B CRC64;
 SQ
 Query Match 8.1%; Score 107; DB 1; Length 211;
 Best Local Similarity 22.2%; Pred. No. 0.051;
 Matches 43; Conservative 27; Mismatches 62; Indels 62; Gaps 7;
 QY 79 EEDIVNLKRGVEPEDLIIISHLHFDHAG----- 111
 DB 32 EGHKINQVKEKGLTP-----LALLTHAFDHIGALDEVREKWDIPVYLHNEKWLADAS 88
 QY 112 --GNGAFINTEPIVQRAEYEAQAQSEYELKECILFNLYKIIEGDEYVPG---VQLLHT 166
 DB 89 LNSGMLRGIEVTAKPADH-----LIEGDGELNIGPFHLETLFT 127
 QY 167 PGHTPGHSLIETKSGPVLITDASYTKENFENVEFPAGFDSLELASSIKRLKEVYMK 226
 DB 128 PGHSPGSVSYV---KADLVISGVLFP--QGGIGRTDLIGNQETLLTSIHE-KLLTLP 181
 QY 227 EKPIVFFGHDIQE 240

DB 182 EHTLVLSGHGPETD 195
 RESULT 12
 YCBL ECOLI STANDARD; PRT; 215 AA.
 ID YCBL ECOLI
 AC Y75849;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein ycbL.
 GN YCBL OR B0927.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RA "The complete genome sequence of Escherichia coli K-12."
 RT Science 277:1453-1474(1997).
 RL [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshina T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sempel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horiuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map."
 RL DNA Res. 3:137-155(1996)
 CC -1- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY. STRONG, TO
 CC H. INFLUENZAE HI1663.
 CC
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 CC
 CC EMBL; AE000195; AAC74013.1; --
 CC EMBL; D90730; BAA35673.1; --
 CC EMBL; D90731; BAA35679.1; --
 CC PIR; F64832; F64832.
 CC EcoGene; EG13704; ycbL.
 CC InterPro; IPR001279; Bactamase-like.
 CC Pfam; PF00753; lactamase B; 1.
 CC Hypothetical protein; Hydrolase; Zinc; Complete proteome.
 CC METAL 56 56 ZINC 1 (BY SIMILARITY).
 CC METAL 58 58 ZINC 1 (BY SIMILARITY).
 CC METAL 60 60 ZINC 2 (BY SIMILARITY).
 CC METAL 61 61 ZINC 2 (BY SIMILARITY).
 CC METAL 132 132 ZINC 1 (BY SIMILARITY).
 CC METAL 151 151 ZINC 1 AND 2 (BY SIMILARITY).
 CC METAL 192 192 ZINC 2 (BY SIMILARITY).
 CC SEQUENCE 215 AA; 23784 MW; C4233FF08308B18D CRC64;
 SQ
 Query Match 8.1%; Score 106.5; DB 1; Length 215;
 Best Local Similarity 26.2%; Pred. No. 0.058;
 Matches 53; Conservative 26; Mismatches 48; Indels 75; Gaps 13;


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QY 79 BEDRVNVL-----KRVGYEPD-----LLYIIISHLHFDHAGNGAFINTPIIVQRAEY 128
Db 21 EQTRIALALVDPGDAEKIKQEVDDSGLTLMQILLTHGLDHSV-----AAA 66
QY 129 EAAQH-----SEBY-----LKEC-----ILPN-----LNYKIIEGDYEVVPGV 161
Db 67 ELAQHYGVVFPPEKEDEFWLGQLPAQSRMFGLECEQPLTPDRWLN-----EGDTISGNV 122
QY 162 ---QLLHTPGHTPGHQSLLIETEK---SGPVLLTTIDASYTKNFENVEVFAFG---DSELA 213
Db 123 TLQVLHCFGHTPGHVHVFDDRAKLISGDVI-----FKGGVGRSDFPRGRDHQL 171
QY 214 LSSIKRLKEVVMKEKPIVFFGH 235
Db 172 ISSIKD-KLLPLGDDVIFPGH 192

RESULT 13
YND2 YEAST
ID YND2 YEAST STANDARD; PRT; 281 AA.
AC P53965;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 32.8 kDa protein in NCE3-HHT2 intergenic region.
GN YNL032W OR N2746.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
SEQUENCE FROM N.A.
RA Duernhoeft A., Floeth M., Fritz C., Heuss-Neitzel D.,
RA Hilbert H., Moestl D.;
RL Submitted (MAY-1996) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: TO YEAST YNL056W AND YNL099C.
CC -----
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CC EMBL; Z71308; CAA95895.1; -.
DR PIR; S62954; S62954.
DR SGD; S0004977; SIW14.
DR GO; GO:0006950; P:response to stress; IGI.
DR InterPro; IPR004861; Put_tyr_phos.
DR Pfam; PF03162; Y_phosphatase2; 1.
DR KW Hypothetical protein.
SQ SEQUENCE 281 AA; 32755 MW; 88BD8AFC620B4570 CRC64;

Query Match 8.0%; Score 105.5; DB 1; Length 281;
Best Local Similarity 20.2%; Pred. No. 0.1;
Matches 51; Conservative 41; Mismatches 71; Indels 89; Gaps 13;

QY 43 EEPFILVDTPGSPASVANNNEGLNFTFVGQVLPQMTBEDRVN-----ILKRV-GYPED 96
Db 36 EDGKLLIDNG-----DGRDIIHQEDKLLSVFNEVLKRFHGEKSD 78
QY 97 LLYIIISHLHFDHAGNGAFINTPIIVQRAEYEAQAQSEVYKECILPNLYKIIEGDYE 156
Db 79 I-----PKREFDEDDG-----YDSNEHHQKTIE---VMNLTNHLVI---NKE 115
QY 157 VVPGVQLLHTPGHT-----PGHQ---SLLIETKSGPVLLITIDASYTKNEFE----- 200
Db 116 VVPPENFHVUVGEIYRSFPRQENFSLHERLKLKSLVLIPEYPOENLFLKLTGKIL 175
QY 201 -----NEVPFAGFDSSELASSIKRLKEVVMK---EKPIVFFGHDIQERGC----- 243
Db 176 YQVGMGSKKEFPNIPSHLLTKAL-----EIVLPANQPILHCNKGHRGCLIGCIRKL 231
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QY 244 -----KVFPEY 249
Db 232 QNWSLTWIFDEY 243

RESULT 14
GL2C ARATH
ID GL2C ARATH STANDARD; PRT; 258 AA.
AC O24496; O04844;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Hydroxyacylglutathione hydrolase cytoplasmic (EC 3.1.2.6) (Glyoxalase
DE II) (Glx II).
GN GLX2-2 OR AT3G10850 OR T7M13.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
SEQUENCE FROM N.A.
RA STRAIN=cv. Wassilewskija;
RX MEDLINE=98009983; PubMed=9349270;
RA Maiti M.K., Krishnasamy S., Owen H.A., Makaroff C.A.;
RT "Molecular characterization of glyoxalase II from Arabidopsis
RT thaliana.";
RN Plant Mol. Biol. 35:471-481(1997).
RN [2]
SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia; TISSUE=Leaf;
RX MEDLINE=97218101; PubMed=9065762;
RA Ridderstroem M., Mannervik B.;
RT "Molecular cloning and characterization of the thiolesterase
RT glyoxalase II from Arabidopsis thaliana.";
RN Biochem. J. 322:449-454(1997).
RN [3]
SEQUENCE FROM N.A.
RA STRAIN=cv. Columbia;
RX MEDLINE=21016720; PubMed=11130713;
RA Salanoubat M., Lemcke K., Rieger M., Ansoerge W., Unseld M.,
RA Fartmann B., Valle G., Bloeker H., Perez-Alonso M., Obermaier B.,
RA Deiseny M., Boutry M., Grivell L.A., Mache R., Puigdomenech P.,
RA De Simone V., Choiane N., Artiguenave F., Robert C., Brottier P.,
RA Wincker P., Cattolico L., Weissenbach J., Saurin W., Quetier F.,
RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Benes V.,
RA Wurmbach E., Drzonek H., Erfle H., Jordan N., Bangert S.,
RA Wiedelmann R., Kranz H., Voss H., Holland R., Brandt P., Nyakatura G.,
RA Vezzi A., D'Angelo M., Pallavicini A., Toppo S., Simonati B.,
RA Conrad A., Hornischer K., Kauer G., Loehner T.-H., Nordsiek G.,
RA Reichelt J., Scharfe M., Schoen O., Barges M., Terol J., Climent J.,
RA Navarro P., Collado C., Perez-Perez A., Ottenwaelder B., Duchemin D.,
RA Cooke R., Laudie M., Berger-Llauro C., Purnelle B., Masuy D.,
RA de Haan M., Maarse A.C., Alcaraz J.-P., Cottet A., Casacuberta E.,
RA Monfort A., Argiriou A., Flores M., Liguori R., Vitale D.,
RA Mannhaupt G., Haase D., Schoof H., Rudd S., Zaccaria P., Mewes H.-W.,
RA Mayer K.F.X., Kaul S., Town C.D., Koo H.L., Tallon L.J., Jenkins J.,
RA Rooney T., Rizzo M., Walts A., Utterback T., Fujii C.Y., Shea T.P.,
RA Creasy T.H., Haas B., Maiti R., Wu D., Peterson J., van Aken S.,
RA Pai G., Miltischer J., Sellers P., Gill J.E., Feldblyum T.V.,
RA Preuss D., Lin X., Nierman W.C., Salzberg S.L., White O., Venter J.C.,
RA Fraser C.M., Kaneko T., Nakamura Y., Sato S., Kato T., Asanizu E.,
RA Sasamoto S., Kimura T., Ideawa K., Kawashima K., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
RA Nakayama S., Nakazaki N., Shinpo S., Takeuchi C., Wada T.,
RA Watanabe A., Yamada M., Yasuda M., Tabata S.;
RT "Sequence and analysis of chromosome 3 of the plant Arabidopsis
RT thaliana.";
RN Nature 408:820-822(2000).
CC -!- FUNCTION: Thiolesterase that catalyzes the hydrolysis of S-D-
CC lactoyl-glutathione to form glutathione and D-lactic acid.
CC -!- CATALYTIC ACTIVITY: (S) - (2-hydroxyacyl)glutathione + H(2)O =
```

```
CC glutathione + a 2-hydroxy acid anion.
CC -!- COFACTOR: BINDS TWO ZINC IONS (BY SIMILARITY).
CC -!- PATHWAY: Glyoxal pathway.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- SIMILARITY: BELONGS TO THE GLYOXALASE II FAMILY.
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CC -----
CC EMBL; U90929; AAC49867.1; -.
CC DR EMBL; Y08357; CAA69644.1; -.
CC DR EMBL; AC011708; AAF19564.1; -.
CC DR HSSP; Q16775; 1QH5.
CC DR InterPro: IPR001279; Blactmase-like.
CC DR Pfam; PF00753; lactamase_B; 1.
CC KW Hydrolase; Zinc.
CC FT METAL 54 54 ZINC 1 (BY SIMILARITY).
CC FT METAL 56 56 ZINC 1 (BY SIMILARITY).
CC FT METAL 58 58 ZINC 2 (BY SIMILARITY).
CC FT METAL 59 59 ZINC 2 (BY SIMILARITY).
CC FT METAL 112 112 ZINC 1 (BY SIMILARITY).
CC FT METAL 135 135 ZINC 1 AND 2 (BY SIMILARITY).
CC FT METAL 174 174 ZINC 2 (BY SIMILARITY).
CC FT METAL 14 14 S -> T (IN REF. 1).
CC FT CONFLICT 85 93 GCTDAVNG -> VALMLRIC (IN REF. 1).
CC FT CONFLICT 98 102 LGQDI -> WSGY (IN REF. 1).
CC FT CONFLICT 122 122 N -> T (IN REF. 1).
CC SQ SEQUENCE 258 AA; 28792 MW; 6703B98A8F902B5A CRC64;

Query Match 7.6%; Score 100.5; DB 1; Length 258;
Best Local Similarity 18.4%; Pred. No. 0.24;
Matches 43; Conservative 33; Mismatches 51; Indels 107; Gaps 9;

QY 93 EPEDLL-----YIISHLHFDHAGNGAFINPTIVQRAEYAAQHSSEYLKEC 141
D 32 DPEKVIASAEKHOAKIKFVLTTHHWDHAGN-----EKTKQ- 68
QY 142 ILPNLNKILTEGVEVVPG-----VQLLHTPGTTPGHQSLLIE-TEK 182
D 69 LVFDI--KVYGGSLDKVKGCTDAVDNGDKLTGLQDINILALHTPCHTKGHISYYVNGKG 126
QY 183 SGFVLLTIDA-----SYTKENFE----- 200
D 127 ENPAVFTGDTLFLVAGCGKFFEGTAEQMYQSLCVTLAALPKPTQVYCGHEVTVKNLEFALT 186
QY 201 -----NEVPFAGFDSALSSIKRLKEVVMKEKPIVFFGH-DIEQERGCK 244
D 187 VEPNNGKIQKLAWARQQRADLPTIPSTILEELETNPFMRVKDPEIQEKLCK 240

RESULT 15
YFBB BACSU
ID YFBB BACSU STANDARD; PRT; 220 AA.
AC P37502;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein yfbb.
GN YFBB.
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX Ogasawara N., Nakai S., Yoshikawa H.;
RA Ogasawara N., Nakai S., Yoshikawa H.;
RT "Systematic sequencing of the 180 kilobase region of the Bacillus

RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moser I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conneron I.F., Cummings N.J., Daniel R.A.,
RA Denicot F., Devigne K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Etian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Chim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardiniois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield P.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Tacconi E., Takagi T., Takanashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";
RL Nature 390:249-256(1997).
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CC DR EMBL; Z99124; CAB16107.1; -.
CC DR PIR; S65995; S65995.
CC DR Subtilist; BG10029; Yybb.
CC DR InterPro: IPR001279; Blactmase-like.
CC DR Pfam; PF00753; lactamase_B; 1.
CC KW Hypothetical protein; Complete proteome.
CC SQ SEQUENCE 220 AA; 25266 MW; 57AF02520BA1A3C5 CRC64;

Query Match 7.6%; Score 99.5; DB 1; Length 220;
Best Local Similarity 23.9%; Pred. No. 0.23;
Matches 43; Conservative 25; Mismatches 63; Indels 49; Gaps 9;

QY 31 LDLPVWCYLLETGEGPILVDTGMPESAVNNEGLFNGTFVSGOVLPMKTEEDRVNILKRV 90
D 21 LRIPVHTWFIKDGDDVIVDTGIER-----FADAQIRALAA-----I 57
QY 91 GYEPEDLLYIISHLHFDHAGNGAFI---NTPIVQRAEYAAQHSSEYLKECILPNLN 147
D 58 G-NPKAILL---THGSDHIGGASKWLERDPIFAHOKELKYNGEPEY-----PNKN 107
QY 148 YKIEGDEYVVPGV---QLLH-----TPGHTPGHQSLLIETKSGPVLITDASYTKE 197
D 108 EVENTGVAHIVQPLTEQTLAHLPLKYLITPGHSPGH---VYVYHKIDRTLLTGDLFITSK 164

Search completed: February 20, 2004, 16:25:12
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Job time : 18 secs

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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:26:08 ; Search time 34 Seconds
(without alignments)
1539.576 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLLFVPAGRCMLDHS.....VFFGHDIQERCKVPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pap.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pap.*
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7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pap.*
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13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pap.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pap.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pap.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	142.5	10.8	249	15	US-10-156-761-9011
3	130.5	9.9	372	15	US-10-156-761-13378
4	123.5	9.4	285	12	US-10-264-237-2716
5	120.5	9.2	378	15	US-10-156-761-7704
6	119	9.0	298	9	US-09-925-301-1224
7	109.5	8.3	274	12	US-10-369-493-1669
8	109	8.3	361	12	US-10-216-163-8
9	109	8.3	361	12	US-10-218-765-8
10	109	8.3	361	12	US-10-219-063-8
11	109	8.3	361	12	US-10-219-066-8
12	109	8.3	361	12	US-10-219-067-8
13	109	8.3	361	12	US-10-219-068-8
14	109	8.3	361	12	US-10-219-069-8
15	109	8.3	361	12	US-10-219-073-8

16	109	8.3	361	12	US-10-219-475-8	Sequence 8, Appli
17	109	8.3	361	12	US-10-219-480-8	Sequence 8, Appli
18	109	8.3	361	12	US-10-219-483-8	Sequence 8, Appli
19	109	8.3	361	12	US-10-219-525-8	Sequence 8, Appli
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21	109	8.3	361	12	US-10-219-530-8	Sequence 8, Appli
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23	109	8.3	361	12	US-10-219-532-8	Sequence 8, Appli
24	109	8.3	361	12	US-10-219-533-8	Sequence 8, Appli
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26	109	8.3	361	12	US-10-232-228-8	Sequence 8, Appli
27	109	8.3	361	12	US-10-232-226-8	Sequence 8, Appli
28	109	8.3	361	12	US-10-230-130-8	Sequence 8, Appli
29	109	8.3	361	15	US-10-227-884-8	Sequence 8, Appli
30	109	8.3	361	15	US-10-230-163-8	Sequence 8, Appli
31	109	8.3	361	15	US-10-230-338-8	Sequence 8, Appli
32	109	8.3	361	15	US-10-218-631-8	Sequence 8, Appli
33	109	8.3	361	15	US-10-230-414-8	Sequence 8, Appli
34	109	8.3	361	15	US-10-216-159A-8	Sequence 8, Appli
35	109	8.3	361	15	US-10-218-849-8	Sequence 8, Appli
36	109	8.3	361	15	US-10-227-873-8	Sequence 8, Appli
37	109	8.3	361	15	US-10-227-883-8	Sequence 8, Appli
38	109	8.3	361	15	US-10-219-076-8	Sequence 8, Appli
39	109	8.3	361	15	US-10-230-434-8	Sequence 8, Appli
40	109	8.3	361	15	US-10-219-003-8	Sequence 8, Appli
41	109	8.3	361	15	US-10-219-075-8	Sequence 8, Appli
42	109	8.3	361	15	US-10-219-464-8	Sequence 8, Appli
43	109	8.3	361	15	US-10-219-466-8	Sequence 8, Appli
44	109	8.3	361	15	US-10-219-479-8	Sequence 8, Appli
45	109	8.3	361	15	US-10-219-481-8	Sequence 8, Appli

ALIGNMENTS

RESULT 1

US-10-156-761-8756
; Sequence 8756, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8756
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8756

Query Match 11.7%; Score 153.5; DB 15; Length 290;
Best Local Similarity 25.7%; Pred. No. 2.5e-07;

Matches 61; Conservative 44; Mismatches 93; Indels 39; Gaps 11;

Qy 37 CYLLETE-BEPIIVDTGMPESAVNNEGLFNGTFTVEQVLPMTTEEDRIVNILKRVGEPE 95
Db 41 CLLVETDRDGLVIVESIGTADVARPEQNLGADFLGRAQPVLDLAETALHQTGLGRPE 100
Qy 96 DLLYITSSHLHFHAGNGAFINTPIVQPAEYEAQ-----HSEYLLKE-----CILPN 145
Db 101 GVRHIVLSHLLDHDAGLSDFPWAKVHLTEAHRRAAAMPAGHPEDKRVRYRPAQWAHRPH 160

146 -LNYKIIIEGD-----YEWV-----GVQLLHTP--GHTPGHQSLLIETKSGPVLLTI-DA 192
161 WVTYEAQGPWFQFADVAPLDGLDAEILLVPLGCHTRGHSALAV--RDTGRWLLHCGDA 218
193 SYTKENFENEVP-----FAGFDSALSSIKRLKEVYMK--EKPIVFFGHD 236
219 YXFHREIDPDPRGHFQMDILOITVDRPLRLGNHARULRELVRHGDVEVFSAMD 275

RESULT 2
US-10-156-761-9011
; Sequence 9011, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, HIROSHI
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 9011
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-9011

Query Match 10.8%; Score 142.5; DB 15; Length 249;
Best Local Similarity 25.4%; Pred. No. 2.7e-06;
Matches 59; Conservative 31; Mismatches 75; Indels 67; Gaps 13;
QY 35 VMCVLLTERGPIIVDTGMPESAVNNEGLFNGTFVGGVQLPKMTEEDRIVNILKRVGVPE 94
Db 32 LWC---DGDES-TLIDAGVGSAA-----IVQALTGIGRRP 64
QY 95 EDLLYIISHLHFDHAGNGAF-----INTPIIVQRAE-----YFAAQ 132
Db 65 EDVRRIVLTHFEDHAGGAGFAALSGARVSAHRLDAPV--RGELPGPPVFDWERP 122
QY 133 HS-----EYKKECIILPNLYKIEGD--YEVVPGVQLLHTPGHTPGHQSLLIETKSGP 185
Db 123 HAGVSKLLPERSPDQVRPEAVAEALSDGVLDFGGGARVHAFGHTAG--SVAFHLPBHG- 179
QY 186 VLLTIDASYTKENFENEVPFAGF--DSEALSSIKRLKEVYMKKEKPIVFFGCH 235
Db 180 VLFTGDA--VAASPVDGRVMLGVFNVDRAQAVDSFRRLASL---DADIACFGH 227

RESULT 3
US-10-156-761-13378
; Sequence 13378, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761

CURRENT FILING DATE: 2002-05-29
PRIOR APPLICATION NUMBER: JP 2001-204089
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: JP 2001-272697
PRIOR FILING DATE: 2001-08-02
NUMBER OF SEQ ID NOS: 15109
SEQ ID NO 13378
LENGTH: 372
TYPE: PRT
ORGANISM: Streptomyces avermitilis
US-10-156-761-13378

Query Match 9.9%; Score 130.5; DB 15; Length 372;
Best Local Similarity 25.8%; Pred. No. 8.6e-05;
Matches 47; Conservative 29; Mismatches 47; Indels 59; Gaps 8;
QY 38 YLLETEGPILVDTGMPESAVNNEGLFNGTFVGGVQLPKMTEEDRIVNILKRVGVPEDL 97
Db 60 YVVDTRGVPVLDTGWDPPASWD-----TLTEG-----LTACGTSAAEI 98
QY 98 LYIISHLHFDHAG-----GNCAFI-----NTPII-----VQRAEYEAQ 132
Db 99 HGVVITHHHDPHGLSGRVREMSGAWTAAHAADTAVVRRTRARPDPWFYMTAKLMAAG 158
QY 133 HSEYEL-----KECILPNL-----NVKIEGDEYEVVPGVQL--LHTPGHTPGHQSLLIE 179
Db 159 APEAHVAPLPAARPRALPGLSPALPDREIVPGDLVGLPGRRLRAIWTGHTPGHVCLE 218
QY 180 TE 181
Db 219 EE 220

RESULT 4
US-10-264-237-2716
; Sequence 2716, Application US/10264237
; Publication No. US20040009491A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA131P1
; CURRENT APPLICATION NUMBER: US/10/264,237
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/16450
; PRIOR FILING DATE: 2001-05-18
; PRIOR APPLICATION NUMBER: US 60/205,515
; PRIOR FILING DATE: 2000-05-19
; NUMBER OF SEQ ID NOS: 2876
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 2716
; LENGTH: 285
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (250)
; OTHER INFORMATION: Xaa equals any of the twenty naturally occurring L-amino acids
US-10-264-237-2716

Query Match 9.4%; Score 123.5; DB 12; Length 285;
Best Local Similarity 25.4%; Pred. No. 0.00031;
Matches 60; Conservative 28; Mismatches 71; Indels 77; Gaps 12;
QY 39 LLETEGPILVDTGMPESAVNNEGLFNGTFVGGVQLPKMTEEDRIVNILKRVGVPEDL 98
Db 76 LEEAARGPILVDTGCPWA-----REALGLACQGNAPGDVT 112
QY 99 YIISHLHFDHAGNGAFINTPIIVQRAEYEAQHSBEYKKECILPNLYKI-----IEGD 154
Db 113 LVVGTGHSDHIGNLGLFPAGALLVSH-----DFCLPGGRYLPGLGGERP 158
QY 155 YEVVPGVQLLHTPGHTPGHQ---SLLIETKSGPVLLTIDASYTKENFENEVPFAGFDE 211

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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (279)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1224

Query Match      9.0%; Score 119; DB 9; Length 298;
Best Local Similarity 24.4%; Pred. No. 0.00096;
Matches 53; Conservative 31; Mismatches 63; Indels 70; Gaps 10;

QY 38 YLLETEEGPLVDVTGMPESAVNNEGLFNGTFVVGQVLPMKTEEDRIIVNILKRVGYRPEDL 97
Db 44 YLVGTGPRRLIDITGEP-----ALPE-----VISCLKQALTEENTA 79
QY 98 LY-IISHLHFDHAGNGAF---INT-----PIIVQRAEYEA-AQHSEYVKECIL 143
Db 80 IQEIVVTHWRDHSGGIGDICKSINNDTTYCIKLPNPQREELIGNGEQQYVYVK--- 135
QY 144 PNLNYKIIIEGDYEVVPG--VOLLHTPGHTPGHOSLLIETEK---SGPVLLTIDASYTKEN 198
Db 136 -----DGDVIKTEGATRLVLYTPGHTDDHMLLEENAIKPSGDCILGEGTTFPEDL 187
QY 199 FENEVPFAGFDSALSSIKRLKEVVMKEKPIVFFGH 235
Db 188 YD-----YMSLKLKADIIYPGH 209

RESULT 7
US-10-369-493-1669
; Sequence 1669, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 1669
; LENGTH: 274
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-369-493-1669

Query Match      8.3%; Score 109.5; DB 12; Length 274;
Best Local Similarity 21.8%; Pred. No. 0.0082;
Matches 50; Conservative 40; Mismatches 82; Indels 57; Gaps 11;

QY 36 WCYLLLETEEG--PILVDITGMPESAVNNEGLFNGTFVVGQVLPMKTEEDRIIVNILKRVGYE 93
Db 17 YCVLLSDSKNKSMLIDPAEPP-----EVLPELDEKI----- 50
QY 94 PEDLLYIISHLHFDHAGNGAFI-----NTPIVQRAEYEAQAQHSSEYVKECILPNLNY 148
Db 51 --SVEAIVNTHHYHADGNADILKVKLNKPN-----TSKVEVITGGSKDCPKVITIIPENLK 104
QY 149 KIIEGDYEVVPGVQLLHTPGHTPGHOSLLIETEKSGP-VLLTIDASYTK--ENFENEVPF 205
Db 105 KHLGDDLEIT-----CINTPCHTRDSICYVVDPTTDERCIFTGDTLFTACGGRF-----F 155
QY 206 AGFDSEALSSIKRLKEVVMKE---KPVFFGHDIQEOR---GCKVPE 248
Db 156 EGTGEEMDIALNNSILETVGRQNSKTRVYPGHEYTSNKNVFKVIYPQ 204

; LENGTH: 298

Db 159 LQLPGLELVATPGH--GGORDSVVVVAGTALGTVVVAGDV-----FERS-----GDEDSW 207
QY 212 LALS-----SIKRL---KEVVM-----KEKPIVFFGHDIQEERG-CKVF 246
Db 208 QALSEDPVAQERSKRKRLVDLTADVVPVPGHAPFRGSEKPL-SHGKDVQKTRGQCDRF 262

RESULT 5
US-10-156-761-7704
; Sequence 7704, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUNOSHI
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 7704
; LENGTH: 378
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-7704

Query Match      9.2%; Score 120.5; DB 15; Length 378;
Best Local Similarity 22.2%; Pred. No. 0.00096;
Matches 43; Conservative 34; Mismatches 74; Indels 43; Gaps 7;

QY 66 GTFVEGQVLPKMTTEEDRIIVNILKRVGYRPEDLVYIISHLHF-----DHA 110
Db 134 GDFLTHVFAFYDPN--TVLPSCGLRPEDVDFVSPFDHLHVQVDMIMGSTRITIPGERA 191
QY 111 GNGAFINTPIIVQRAEYEAQAQHSSE-----YLKECI--LPNLNYKIIIEGDYEVVPGVQL 163
Db 192 PREALFPARLLVHRRELGTFTSTHPQWAWYVDGMDGVPPERVATPDGVDVLGVGVS 251
QY 164 LHTPGHTPGHOSLLIETEKSGPVLITIDASYTKENFENFENFVFPAGFDSALSSIKRLKEV 223
Db 252 LWTFGHTDGNHSLVLTDPG--VWVSSENGISADNWQPE-----LSRIPGVR-- 296
QY 224 VMKEKPIVFFGHDI 237
Db 297 ---RHAAFYGEV 306

; LENGTH: 298

RESULT 6
US-09-925-301-1224
; Sequence 1224, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1224
; LENGTH: 298
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RESULT 8
US-10-216-163-8
; Sequence 8, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C3
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04

; Sequence 8, Application US/10218765
; Publication No. US20030187201A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C19
; CURRENT FILING DATE: 2002-08-12
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; PRIOR APPLICATION NUMBER: 60/081819
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/081955
; PRIOR FILING DATE: 1998-04-15
; PRIOR APPLICATION NUMBER: 60/082804
; PRIOR FILING DATE: 1998-04-22
; PRIOR APPLICATION NUMBER: 60/084441
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/085323
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/089532
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089905
; PRIOR FILING DATE: 1998-06-18
; PRIOR APPLICATION NUMBER: 60/090472
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090557
; PRIOR FILING DATE: 1998-06-24
; PRIOR APPLICATION NUMBER: 60/090691
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/090695
; PRIOR FILING DATE: 1998-06-25
; PRIOR APPLICATION NUMBER: 60/091982
; PRIOR FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: 60/095302
; PRIOR FILING DATE: 1998-08-04
; PRIOR APPLICATION NUMBER: 60/095318
; PRIOR FILING DATE: 1998-08-04

Query Match      8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNQTVGVGVQLPKMTEDRIVNLI-----KRVGVPEP-----LLVVIS 102
Db 91 LFNQV-----KVLPIVLSNYSVLIIDTQQLAVAVDPSPRAVQASIEKGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYLKBCI-----LPLNLYKIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVGSPQDGPVYLTHPLCHQD 188
QY 155 YEVVPGVOL--LHTPGHTPHQSLLIETEK-----SGPVLLITDASTKENFENVP 204
Db 189 VWSVGLQIRALATPCHGTQGHVLLDGEYPKGFSCILFSGDLLFLSCGRTFEG----- 242
QY 205 FAGFDSLSLSSIKRLKEVVMKPIVFFGHGHDIEQ 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLMLPCHYEAE 272

; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-216-163-8

Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
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Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYABE 272

RESULT 10
US-10-219-063-8
; Sequence 8, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-063-8

Query Match 8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

Qy 63 LFNQTFVEGQVLPKMTEDRIVNLT-----KRVGYEPED-----LLYIIS 102
Db 91 LFNQV----KVLPIPLSDNYSYLIIDTQALAVADPSDPRAVQASIEKEGVTILAILC 146

Qy 103 SHLHFDHAGNGAFINTPIIVQAEYEAQHSEYVLEKCI-----LPLNLYKILLEGD 154
Db 147 THKHWDSHGGNRDL-----SRRH-----RDCRVYGPQDGIPVLTPLCHQD 188

Qy 155 YEVVPGVQL--LHTPGHTPGHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204
Db 189 VVSVGRQLIRALATPGHTQGHVYLLDGEPPYKGPSCLFSGDLLFLSGCGRTFEG-----242

Qy 205 FAGFDSSEALSSIKRLKEVVMKKEPIVFFGHDIQEQ 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYABE 272

RESULT 12
US-10-219-067-8
; Sequence 8, Application US/10219067
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Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYABE 272

RESULT 10
US-10-219-063-8
; Sequence 8, Application US/10219063
; Publication No. US20030187202A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C24
; CURRENT APPLICATION NUMBER: US/10/219,063
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-063-8

Query Match 8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

Qy 63 LFNQTFVEGQVLPKMTEDRIVNLT-----KRVGYEPED-----LLYIIS 102
Db 91 LFNQV----KVLPIPLSDNYSYLIIDTQALAVADPSDPRAVQASIEKEGVTILAILC 146

Qy 103 SHLHFDHAGNGAFINTPIIVQAEYEAQHSEYVLEKCI-----LPLNLYKILLEGD 154
Db 147 THKHWDSHGGNRDL-----SRRH-----RDCRVYGPQDGIPVLTPLCHQD 188

Qy 155 YEVVPGVQL--LHTPGHTPGHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204
Db 189 VVSVGRQLIRALATPGHTQGHVYLLDGEPPYKGPSCLFSGDLLFLSGCGRTFEG-----242

Qy 205 FAGFDSSEALSSIKRLKEVVMKKEPIVFFGHDIQEQ 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYABE 272
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; Publication No. US20030187204A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C31

; CURRENT APPLICATION NUMBER: US/10/219,067

; PRIOR FILING DATE: 2002-08-14

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 8

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-219-067-8

Query Match 8.3%; Score 109; DB 12; Length 361;

Best Local Similarity 22.7%; Pred. No. 0.014;

Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNCTFVEGVQLPKMTEDRIVNLT-----KRVGYEPED-----LLYIIS 102

Db 91 LFNQV----KVLPIPLVSDNYSLIIDTQQLAVAVDPSPRAVQASIEKEGVTVAIIC 146

QY 103 SHLHFDHAGNGAFINPTPIIVQRAEYEAQHSEYELKECI-----LPLNLYKIIEGD 154

Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQDGPVLTPLCHQD 189

QY 155 YEVVPGVQL--LHTPGTPOHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204

Db 189 VVSVGRQLIRALATPGTQGHVLLDGEYPYKGFSCFLSGDGLFLSGCGRTFEG-----242

QY 205 FAGFDSSEALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240

Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

RESULT 13

US-10-219-068-8

; Sequence 8, Application US/10219068

; Publication No. US20030187205A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Grimaldi, J. Christopher

; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin L.

; APPLICANT: Wood, William I.

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; FILE REFERENCE: P3530P1C31

; CURRENT APPLICATION NUMBER: US/10/219,068

; CURRENT FILING DATE: 2002-08-13

; PRIOR APPLICATION NUMBER: 10/119,480

; PRIOR FILING DATE: 2002-04-09

; PRIOR APPLICATION NUMBER: 60/059113

; PRIOR FILING DATE: 1997-09-17

; PRIOR APPLICATION NUMBER: 60/062287

; PRIOR FILING DATE: 1997-10-17

; PRIOR APPLICATION NUMBER: 60/063549

; PRIOR FILING DATE: 1997-10-28

; PRIOR APPLICATION NUMBER: 60/064103

; PRIOR FILING DATE: 1997-10-31

; PRIOR APPLICATION NUMBER: 60/069873

; PRIOR FILING DATE: 1997-12-17

; PRIOR APPLICATION NUMBER: 60/078910

; PRIOR FILING DATE: 1998-03-20

; PRIOR APPLICATION NUMBER: 60/079294

; PRIOR FILING DATE: 1998-03-25

; PRIOR APPLICATION NUMBER: 60/079656

; PRIOR FILING DATE: 1998-03-26

; PRIOR APPLICATION NUMBER: 60/079728

; PRIOR FILING DATE: 1998-03-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 246

; SEQ ID NO 8

; LENGTH: 361

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-219-068-8

Query Match 8.3%; Score 109; DB 12; Length 361;

Best Local Similarity 22.7%; Pred. No. 0.014;

Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;

QY 63 LFNCTFVEGVQLPKMTEDRIVNLT-----KRVGYEPED-----LLYIIS 102

Db 91 LFNQV----KVLPIPLVSDNYSLIIDTQQLAVAVDPSPRAVQASIEKEGVTVAIIC 146

QY 103 SHLHFDHAGNGAFINPTPIIVQRAEYEAQHSEYELKECI-----LPLNLYKIIEGD 154

Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQDGPVLTPLCHQD 188

QY 155 YEVVPGVQL--LHTPGTPOHQSLLIETEK-----SGPVLITIDASYTKENFENEVP 204

Db 189 VVSVGRQLIRALATPGTQGHVLLDGEYPYKGFSCFLSGDGLFLSGCGRTFEG-----242

QY 205 FAGFDSSEALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240

Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

RESULT 14

US-10-219-069-8

; Sequence 8, Application US/10219069

; Publication No. US20030187206A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Desnoyers, Luc

; APPLICANT: Gerritsen, Mary

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C40
; CURRENT APPLICATION NUMBER: US/10/219,069
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-069-8

Query Match 8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;
QY 63 LFNQTFVEGVQLPKMTTEEDRIVNLI-----KRVGYEPED-----LXYIIS 102
Db 91 LFNQV-----KVLPIPVLSNYSYLIIDTQALAVAVDPSPRAVOASIEKEGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYKKECI-----LPLNLYKIIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQPDGIPYLTHPLCHQD 188
QY 155 YEVVPGVQL--LHPTGHTPGHQSLLIETEK-----SGVLLTTIDASYTKENFENEVP 204
Db 189 VWSVGRLOIRALATPGHTQGHLYVLDGEPYKPSCLFSGDLLFLSCGRTFEG-----242
QY 205 FAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

RESULT 15

US-10-219-073-8
; Sequence 8, Application US/10219073
; Publication No. US20030187207A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.

; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C52
; CURRENT APPLICATION NUMBER: US/10/219,073
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 8
; LENGTH: 361
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-219-073-8

Query Match 8.3%; Score 109; DB 12; Length 361;
Best Local Similarity 22.7%; Pred. No. 0.014;
Matches 49; Conservative 33; Mismatches 62; Indels 72; Gaps 10;
QY 63 LFNQTFVEGVQLPKMTTEEDRIVNLI-----KRVGYEPED-----LXYIIS 102
Db 91 LFNQV-----KVLPIPVLSNYSYLIIDTQALAVAVDPSPRAVOASIEKEGVTLVAILC 146
QY 103 SHLHFDHAGNGAFINTPIIVQRAEYEAQHSSEYKKECI-----LPLNLYKIIEGD 154
Db 147 THKHWDHSGGNRDL-----SRRH-----RDCRVYGSQPDGIPYLTHPLCHQD 188
QY 155 YEVVPGVQL--LHPTGHTPGHQSLLIETEK-----SGVLLTTIDASYTKENFENEVP 204
Db 189 VWSVGRLOIRALATPGHTQGHLYVLDGEPYKPSCLFSGDLLFLSCGRTFEG-----242
QY 205 FAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
Db 243 ----NAETMLSSLDTV--LGLGDDTLLWPGHEYAE 272

Search completed: February 20, 2004, 16:31:37
Job time : 36 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 20, 2004, 16:23:12 ; Search time 20 Seconds
(without alignments)
1202.109 Million cell updates/sec

Title: US-10-019-661-2
Perfect score: 1315
Sequence: 1 MTVKLYFVAGRCMLDHS.....VFFGHDIEQERGCKVFPEYI 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR.76:*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	299	22.7	256	AG3176	Zn-dependent hydro
2	260	19.8	269	G90312	conserved hypot
3	251	19.1	301	G84288	hypothetical prote
4	242.5	18.4	262	D69438	hypothetical prote
5	236	17.9	271	D75552	conserved hypot
6	233.5	17.8	276	AE3236	Zn-dependent hydro
7	210	16.0	279	E82689	conserved hypot
8	186	14.1	253	G75350	conserved hypot
9	183.5	14.0	280	G89959	conserved hypot
10	172.5	13.1	205	D69036	conserved hypot
11	157	11.9	310	H70733	hypothetical prote
12	156.5	11.9	333	AH2652	metallo-beta-lacta
13	156.5	11.9	370	E97434	hypothetical prote
14	156	11.9	284	D84057	hypothetical prote
15	152	11.6	203	A64337	hypothetical prote
16	151	11.5	304	T37060	hypothetical prote
17	147	11.2	324	F95386	protein [imported
18	145.5	11.1	275	AH0443	conserved hypot
19	145.5	11.1	283	AF1276	hypothetical prote
20	145	11.0	282	AF1639	hypothetical prote
21	143.5	10.9	209	G69321	conserved hypot
22	143.5	10.9	248	C83865	hypothetical prote
23	143	10.9	218	F72272	conserved hypot
24	143	10.9	223	G71064	hypothetical prote
25	141	10.7	222	B75083	probable hydroxyc
26	141	10.7	302	A84357	hypothetical prote
27	141	10.7	335	AG3085	conserved hypot
28	141	10.7	335	B98201	hypothetical prote
29	139.5	10.6	251	F86942	conserved hypot

30 137.5 10.5 233 2 E90315 conserved hypot

31 137.5 10.5 235 2 E90473 hypothetical prote

32 135.5 10.3 324 2 F84719 probable glyoxalase

33 135 10.3 213 2 A90269 conserved hypot

34 135 10.3 264 2 D69811 hypothetical prote

35 135 10.3 319 2 G95282 conserved hypot

36 134.5 10.2 236 2 C69468 conserved hypot

37 134.5 10.2 310 2 G90423 conserved hypot

38 133.5 10.2 209 2 G72321 conserved hypot

39 133.5 10.2 319 2 AB3170 metallo-beta-lacta

40 133 10.1 204 2 A75189 hypothetical prote

41 132 10.0 215 2 D75342 conserved hypot

42 130.5 9.9 198 2 F71229 hypothetical prote

43 130.5 9.9 236 2 B83879 hypothetical prote

44 128.5 9.8 256 2 G69997 hypothetical prote

45 127 9.7 211 2 D84002 hypothetical prote

ALIGNMENTS

RESULT 1

AG3176
Zn-dependent hydrolases [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plas
C:Species: Agrobacterium tumefaciens
C:Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AG3176
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McGlell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm, I
ster, E.W.
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AG3176
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-256 <KUR>
A:Cross-references: GB:AE008687; PIDN:AAL45829.1; PID:gl7743569; GSPDB:GN00188
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: attM
A:Genome: plasmid

Query Match 22.7%; Score 299; DB 2; Length 256;
Best Local Similarity 31.7%; Pred. No. 1.4e-17;
Matches 80; Conservative 47; Mismatches 105; Indels 20; Gaps 8;
Qy 13 RCLDHSNSTLTPGELLDPWCYLLETEEGPILVDTCMP-ESAVNNGLFNGTFVEG 71
Db 8 KCKVHNKMQ--GNGADYEIPVFFLIHPAGHTVIDGNAIEVATDPRHMG--ICD 63
Qy 72 QVLPKMTEDRIYNIILKRVGYEPEDLLYLISSHLHFDHAGNGAFINTPIIVQAEYEA 131
Db 64 VYFVLDDKGGVDQIKALGDFADVKYVQSHLLDHTGAIGRFPNATHIVQSEYEA 123
Qy 132 QHSEYI-----KECILPNLYKIIEG---DYEVVEG---VQLLTPGHTPGHQSLIE 179
Db 124 FTDWFAAGGYIRKDPKGLKWOFLNGAODDYVYVGDGTLTITFTPGHAPGHQSLVR 183
Qy 180 TEKSGPVLITIDASYKENFENEPFAGFDSGL--ALSSIKRLKEVVMKEKPIVFFGHDI 237
Db 184 LPNSKELLITIDAAITLDHWE-EKALPGFLASTVDTVRSVQKLRTYAEKHDATVVTGHP 242
Qy 238 EQERGCKVFPEY 249
Db 243 DAWANFKKAPF 254

RESULT 2

G90312
conserved hypothetical protein [imported] - Sulfolobus solfataricus

```

111 FHED-----ADEHTLPAALADAGTAISDIDAVVASHLHLHDHAGGLRHFAGTDPPIYVH 169
      |-----EAOHSSEYLKECILPNINXYKI---EGDYEVVPGVQLLHTRPGH
125 RABY-----
      |      |||:::|      |||:::|      |||:::|      |||
165 ERELGYAYRSAATDGTGSIAYHSPDFRA-----LNRVVAVDRRRQQLPGGLDLHLDPGH 219
      |      |||:::|      |||:::|      |||:::|      |||
170 TPQHQSLLITEK-SGPVLITIDASYTKENPENEVPEA-GFDSELA--LSSIKRLKEVVM 225
      |||:::|      |||:::|      |||:::|      |||:::|      |||:::|
220 TPGILGLYLEPEDGAAPVAGDEAYQRENYEDGVPMTSLLSLADWRESRRRVRLDAR 279
      |      |||:::|      |||:::|      |||:::|      |||:::|
226 KEKPIVFFGHD 236
      :      |||:::|      |||:::|      |||:::|      |||:::|
280 RTTADVFCGHD 290

```

```

RESULT 4
D69438
hypothetical protein AF1509 - Archaeoglobus fulgidus
C:Species: Archaeoglobus fulgidus
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C:Accession: D69438
R:Klenk, H.P.; Clayton, R.A.; Tomb, J.F.; White, O.; Nelson, K.E.; Ketchum, K.A.;
  Glöckner, R.D.; Quackenbush, J.; Lee, N.H.; Sutton, G.G.; Gill, S.; Kirk-
  land, J.F.; Fleischmann, R.D.; Overbeek, J.; Gocayne, J.D.; Weidman, J.F.; McDonald, L.;
  Llave, C.; Zhou, L.; Olsen, G.J.; Adams, M.D.; White, O.; Karp, P.;
  Nature 390, 364-370, 1997
A:Authors: Uterback, T.; Cotton, M.D.; Spriggs, T.; Artiach, P.; Kaine, B.P.;
  Smith, H.O.; Woese, C.R.; Venter, J.C.
A:Title: The complete genome sequence of the hyperthermophilic, sulfate-reduci-
  A:Reference number: A69250; MUID:96049343; PMID:9389475
A:Accession: D69438
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-262 <KLE>

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QY	93	EPEDLLYIISSHLFHEDHAGGNGAFINTPIIVQRAEYEA-----OHSEYLKECILP--N	145
D6	82	KPEDVDKLLIITLHFHDAANAALFTNARIYYQKREWESALNPDLPHRYQTYDSSMLYPLEE	141
QY	146	LNXYKIEGDIYEWPGVQLLHTPGTTPGHQSLLIETEKSPVLITTDASVTKNF-----	199
D6	142	MDCLIIDGDVIAEGVKAVLLPGHTKGIOGVAVETK-GTYLLADHFTYTFNFFPPKQP	200
QY	200	-----ENEYPF--AGPDSLALSSIKRLKEVVMKEKPIVFFGHDIQBERG	243
D6	201	IQMTDTAGNTVEIPTSLPFLPPGLHVLDSIEWEYCFKALSVAKKANILPGHDPGLEG--	258
QY	244	KVFP	247
D6	259	KVFP	262

C:Species: Deinococcus radiodurans
C:date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C:Accession: D75552
R:White, O.; Easen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson
M.; Shen, M.; Vanathavan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zaleski
S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans
A:Reference number: A75250; MUID:20036896; PMID:10567266
A:Accession: D75552

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-271 <WHI>
A;Cross-references: GB:AE001879; GB:AE000513; NID:g6457832; PIDN:AAF09759.1; PID:g645783
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR0172
A;Map position: 1

Query Match 17.9%; Score 236; DB 2; Length 271;
Best Local Similarity 27.0%; Pred. No. 2.9e-12;
Matches 71; Conservative 50; Mismatches 100; Indels 42; Gaps 9;

Qy 3 VKKLYFVAGRCMLDHSVNSTLTPGELLDPVWCYLLETEGPIILVDTGMPESAVNNEG 62
Db 16 VKSFLRPEQNLL--GSLRSFLRQYSAPLFWCMLIEHPSGLIVDTGTCTARSN-- 71
Qy 63 LFNGTFVEGQVLPKMTEDRIVNLKRVGYEPEDLLYIISHLHFDHAGNGAFINTPII 122
Db 72 ---WFSRTQRLHYTEHDLRSQMRAGFPQVRVLLTHLHLDHGRMGDPPEAHL 127
Qy 123 VORAE-----YEAQHSEYLYKECILPNLYKIIEGDEYEVVPGVQLL 164
Db 128 VSARELDYRSLARLMGYSAPTWKSVPHAAPFLPLAHGPPRESADVMGDGRVL---LL 183
Qy 165 HTPGHTPGHOSLLIETKSGPVLITIDASYTKENFENE-----VPFAGFDSALSLIKR 219
Db 184 PTPGHTPGHLSVLR-QFGHDLLAGDLTYSEQDLRTGRIGGIVP-----SPHHRKSMRQ 238
Qy 220 LKEVVMKEKPIVFF-GHDIEQER 241
Db 239 VRQLA-QLRPLIYLPSPHDPDSLR 260

RESULT 6

AE3236
Zn-dependent hydrolases [imported] - Agrobacterium tumefaciens (strain C58, Dupont) plas
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE3236
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE3236
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-276 <KUR>
A;Cross-references: GB:AE008690; PIDN:AAL46307.1; PID:gl7744092; GSPDB:GN00189
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: attM
A;Genome: plasmid

Query Match 17.8%; Score 233.5; DB 2; Length 276;
Best Local Similarity 27.9%; Pred. No. 4.8e-12;
Matches 76; Conservative 42; Mismatches 105; Indels 49; Gaps 12;

Qy 5 KLYFVAGRCMLDHSV--NST-LTP-----GELLDPVWCYLLETEGPIILVDTGM-P 54
Db 4 KLFVLDLGEIRVDENFIANSFTFPKPTVSSRLDIPVSAYLIQCTATVLYDTGCHP 63
Qy 55 ESAVNN-----EGLFNGTFVEGQVLPMTEDRIVNLKRVGYEPEDLLYIISHLHFDH 109
Db 64 ECMGTNGRWAQQLNAPYIG-----ASECNLPKRLQGLSPDDISTVLSHLHNDH 116
Qy 110 AGNGAPINTPIIVQRAEYEA-----QHSBEYLKECILPNL-----NYKII---EGDY 155
Db 117 AGCVFVGKSRLLAHEDEFATVRYFATGHSPPYIVKDIEMLATPRNWDIVGRDER 176

Qy 156 EVPFGVQLLH-TPGHTPGHOSLLIETKSGPVLITIDASYTKENFENVPFA-----G 207
Db 177 ELAPGVNLLFGTGHASGMLGLAVLEKPGFLLVSDACTATYATNPPARRAGVLHDTIG 236
Qy 208 FDSALUSSIKRLKEVVMKEKPIVFGHDIREQ 239
Db 237 YD-----RTVSHIRQYAESRLTVLFGHDIREQ 263

RESULT 7

EB2689
conserved hypothetical protein XF1361 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: EB2689
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: AB2515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: EB2689
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-279 <SIM>
A;Cross-references: GB:AE003968; GB:AE003849; NID:g9106363; PIDN:AAF84170.1; GSPDB:GN001:
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.B.; Kuramae, E.E.; Laigre
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mencia, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1361

Query Match 16.0%; Score 210; DB 2; Length 279;
Best Local Similarity 28.2%; Pred. No. 4.5e-10;
Matches 67; Conservative 39; Mismatches 82; Indels 50; Gaps 10;

Qy 33 LPVWCYLLETEGPIILVDTG-----MPESAVNNEGLFNGTFVEGQVLPMTTEDR 82
Db 44 LPVCFLEIHEPGRFLVDTGDTWRNSIPGYLPRW-----NPLTKQVIVKVALHEE 94
Qy 83 IVNILKRVGYEP-EDLLYIISHLHFDHAGNGAFINTPIIVQRAEYEA----- 131
Db 95 IGPQLLAKNIDPSRDVEAVILTHMHHDHAGLDHFPHTRIIVTKENYDASRGFFGRVAGC 154
Qy 132 --QHSBEYLK-ECILPN-----LNYKII-EGDYEVVPGVQLLHTPGHTPGHOSLLIE 179
Db 155 LPQHPWPLWKPELIETPGAVGPFASSYPITRGRIVLP-----TPGHVKGHVSLVR 208
Qy 180 TEKSGPVLITIDASYTKENFEN-EVPFAGFDSALSLIKRLKEVVMKEKPIVFFGHD 236
Db 209 NDDLSS-IFAGDATYAEIDLRSKGVDTFDPVLSKDTLLRRIETATSTPTTVPMSHD 265

RESULT 8

G75350
conserved hypothetical protein - Deinococcus radiodurans (strain R1)
C;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000
C;Accession: G75350
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; F
, M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma

S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A;Title: Genome sequence of the radioresistant bacterium *Deinococcus radiodurans* R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: G75350
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-253 <WHI>
A;Cross-references: GB:AE002022; GB:AE000513; NID:g6459590; PIDN:AAF11372.1; PID:g6459595
A;Experimental source: strain R1
C;Genetics:
A;Gene: DR1823
A;Map position: 1

[illegible]

RESULT 9
G89959
conserved hypothetical protein SA1568 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: G89959
C:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: R89758; MUID:21311952; PMID:11418146
A:Accession: G89959
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-280 <KUR>
A:Cross-references: GS:BA000018; PTD:gl3701542; PIDN:BA842836.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1568

[illegible]

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Db      203 HMGDIPTTAHKNPLWWTAYD-DYPMQSIRE-----KBRMIPYF---IQQQ 244
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RESULT 10
D69036 conserved hypothetical protein MTH1267 - Methanobacterium thermoautotrophicum (strain Delta H) [Bacteroidetes]
C/Species: Methanobacterium thermoautotrophicum
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 22-Oct-1999
C/Accession: D69036
R/Smith, D.R.; Doucette-Stamm, L.A.; Deloughery, C.; Lee, H.; Dubois, J.; Aldredge, T.; Qi, D.; Spadafora, R.; Vicaire, R.; Wang, Y.; Wierzbowski, J.; Gibson, R.; Jiwani, N. J.; Church, G.M.; Daniels, C.J.; Mao, J.; Rice, P.; Noelling, J.; Reeve, J.N.
A/Bacteriol. 179, 7135-7155, 1997
A/Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: function, gene organization, and phylogenetic analysis
A/Reference number: A69000; MUID:98037514; PMID:9371463
A/Accession: D69036
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-205 <MTH>
A/Cross-residues: GB:AEO00893; GB:AEO00666; MID:g2622375; PIDN:AAB85756.1; PID:g2622375
A/Experimental source: strain Delta H
C/Genetics:
A/Gene: MTH1267
A/Superfamily: glyoxalase

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[illegible]

RESULT 11

H70733
hypothetical protein Rv2300c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: H70733
R:Coile, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Comor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: H70733
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-310 <CON>
A:Cross-references: GB:Z77163; GB:AL123456; NID:G3261610; PIDN:CAB00971.1; PID:e255162;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2300c

Query Match	11.9%	Score 157;	DB 2;	Length 310;
Best Local Similarity	25.7%	Pred. NO. 1.4e-05;		
Watched	62.	Conservative	34;	Mismatches 87;
			Indels	58; Gaps 11;

Search completed: February 20, 2004, 16:26:33
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

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Run on: February 20, 2004, 16:24:07 ; Search time 21 Seconds
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        503.701 Million cell upda
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Title: US-10-019-661-2
Perfect score: 1315
Sequence: 1 MTVKLYFVPAGRCMLDHSS.....VFFGHDIQERGCKVFPEYI 250

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters:	328717
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: /cgn2_6/ptodata/1/iaa/5A COMB pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB pep.*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1 pep.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	180	13.7	311	4	US-09-328-352-5381	Sequence 5381, Ap
2	132.5	10.1	326	4	US-09-328-352-5506	Sequence 5506, Ap
3	128	9.7	722	4	US-09-252-991A-34102	Sequence 24102, A
4	117.5	8.9	295	4	US-09-252-991A-20572	Sequence 20572, A
5	114.5	8.7	239	4	US-09-107-532A-5174	Sequence 5174, Ap
6	106	8.1	209	4	US-09-134-001C-3637	Sequence 3637, Ap
7	101	7.7	290	4	US-09-252-991A-18490	Sequence 18490, A
8	90.5	6.9	724	1	US-08-121-713D-62	Sequence 62, Appl
9	90.5	6.9	724	1	US-08-835-268-62	Sequence 62, Appl
10	90.5	6.9	724	2	US-09-060-692-62	Sequence 62, Appl
11	90.5	6.9	724	3	US-08-833-391-62	Sequence 62, Appl
12	90.5	6.9	724	4	US-09-060-610-62	Sequence 62, Appl
13	90.5	6.9	724	5	PCT-US94-10151A-62	Sequence 62, Appl
14	89	6.8	262	1	US-08-738-944-50	Sequence 50, Appl
15	89	6.8	262	3	US-09-263-352-40	Sequence 40, Appl
16	88.5	6.7	217	4	US-09-252-991A-29680	Sequence 29680, A
17	86.5	6.6	265	4	US-09-198-452A-945	Sequence 945, App
18	85.5	6.5	440	4	US-09-134-001C-5641	Sequence 5641, Ap
19	85	6.5	515	4	US-09-107-532A-6749	Sequence 6749, Ap
20	84	6.4	254	3	US-09-013-881-8	Sequence 8, Appl
21	84	6.4	254	4	US-09-612-473-8	Sequence 8, Appl
22	84	6.4	704	4	US-09-328-352-5144	Sequence 5144, Ap
23	84	6.4	1268	4	US-08-506-296B-28	Sequence 28, Appl
24	84	6.4	15281	2	US-08-471-119A-2	Sequence 2, Appl
25	83.5	6.3	844	4	US-09-564-805-227	Sequence 227, App
26	83.5	6.3	1214	2	US-08-231-193A-54	Sequence 54, Appl
27	83.5	6.3	1214	2	US-08-486-273A-54	Sequence 54, Appl

ALIGNMENTS

```

RESULT 1
US-09-328-352-5381
; Sequence 5381, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: GARY L. BRETON et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 5381
; LENGTH: 311
; TYPE: PR1
; ORGANISM: Acinetobacter baumannii
US-09-328-352-5381

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Query Match	13.7%	Score 180;	DB 4;	Length 311;	
Best Local Similarity	27.1%;	Pred. No. 6.5e-11;			
Matches	69;	Conservative 43;	Mismatches 72;	Indels 72;	Gaps 14;
QY	37	CYLLETEEGPILVDITGMPESAVNNEGLFN-----GTFFVE--GOVLPRKMTTEEDRIVNI	86		
DB	75	CLLVETDRGLVLDITGF-----GLQDYLHMQRGLSLVKRGLKIEPNL--EFSALQQ	124		
QY	87	LKRVGVEPEPLLVIISHLHFDHAGNGAFTNPITIVORAEYEAQAHSSEVLKCEIIPNL	146		
DB	125	IQKLGFHPKDVQHI FVTHLDFDHAGGISDFPHATVHVLALEYNAQ-----LPNF	174		
QY	147	NYKI-----IEGD-----YEVVPGV-----QLLHTP--GHTPGHOSLL	177		
DB	175	KGRLRYRTNOYKQHYWNFVEYQOGKEWFLKVKGPPFLQDEILMVPLLGHSAGHCIA	234		
QY	178	IETKSGPVLITDASVT--KENFEN-----EVPFFAGFDELSALSSIKRLKEVVMKE	227		
DB	235	IKOONOW--LLFCGDAYYSHUELNPAKKRLSLSLEKTFAB--DNEKRLINLKKLQHLQAHE	292		
QY	228	KPI-VFFGHDIEQER	241		
DB	293	PTIEIICADHPHEL	307		

RESULT 2
US-09-328-352-5506
; Sequence 5506, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND

```

RESULT 5
US-09-107-532A-5174
; Sequence 5174, Application US/09107532A
; Patent No. 6583275
;
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
;
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
;
; NUMBER OF SEQUENCES: 7310
;
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354

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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Ariniello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 5174:
SEQUENCE CHARACTERISTICS:
LENGTH: 239 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: YES
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...239
SEQUENCE DESCRIPTION: SEQ ID NO: 5174:

US-09-107-532A-5174

Query Match 8.7%; Score 114.5; DB 4; Length 239;
Best Local Similarity 21.4%; Pred. No. 0.00042;
Matches 62; Conservative 43; Mismatches 80; Indels 105; Gaps 15;
QY 4 KKLFFVAGRC--MLDSSVN-----STLPGELLDLPVWCYLLETEEGPILVDTG 52
DB 5 KLLFLFSPNECVILMDERSFGQGMHIERLKTGMEEN---CYLVYNEALLIIDPG 61
QY 53 MPESAVNNEGLFNGTFVEGVLPKMTEDRIWNILKRVGYEPEDLLYIISHLHFDHAG 112
DB 62 -----EDAERIKQBIKKTNOQP---VAILLTHTHYDHIGA 93
QY 113 ---NGAFINTP-----IIVQAEVRAAQHSEEVYKE 140
DB 94 VEPLRAYQIPVYVSPLEQKWLGPILNLSGLGRHDDIADVISPAYEFE-----MKT 147
QY 141 CILPLNLYKIEGYEVVPGVQLLHTPGHTGHQSLLIETEKSGPVLITDASYTKENFE 200
DB 148 YTLGNMGR-----VVP-----TPCHSIGSVSFID-----DFVVGDLPRGSIGR 189
QY 201 NEVPEAGDSFELASSIKRLKEVVMKEKPIVFFGH-----DIEQERGCKVP 246
DB 190 TDL--ITG-NLEQLHLSI-RTQLFVLDPFEFVYPGHGDATTIEQEKRTNPF 236

RESULT 6

US-09-134-001C-3637
; Sequence 3637, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134,001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08

; PRIOR APPLICATION NUMBER: US 60/055,779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 3637
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3637

Query Match 8.1%; Score 106; DB 4; Length 209;
Best Local Similarity 25.0%; Pred. No. 0.0028;
Matches 42; Conservative 26; Mismatches 56; Indels 44; Gaps 9;
QY 23 STLPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNGTFVEGVLPKMTEDR 82
DB 6 SNLTG-IVDTNT--YFTIENEVLID--PSS-----ESQK 37
QY 83 IWNILKRVGYEPEDLLYIISHLHFDHAGNGAFI---NTPIIVQAEYF-----AA 131
DB 38 IIKKLNQIN--KPLKAILLTHAHYDHIGALDNIIEKYQVVPVYMSKDFDLTDPDKNGS 94
QY 132 QHSEYILKECILPNLN-YKIEGDEVVVP-GVQLLHTPGHTPGHQSLL 177
DB 95 SKFTQYGLSKIESHANPLSLSEGAETEGFKVKVLTHTPGHSPGSLSFV 142

RESULT 7

US-09-252-991A-18490
; Sequence 18490, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 18490
; LENGTH: 290
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18490

Query Match 7.7%; Score 101; DB 4; Length 290;
Best Local Similarity 20.7%; Pred. No. 0.016;
Matches 57; Conservative 37; Mismatches 106; Indels 76; Gaps 12;
QY 13 RCLMDHSSVNSTLTPGELLDLPVWCYLLETEEGPILVDTGMPESAVNNEGLFNG----- 66
DB 52 RVLSSHFAV-----LIEHHAATLLFDGLGRDI---DAQFRADMPWMA 91
QY 67 --TFVEGVLPKMTEDRIWNILKRVGYEPEDLLYIISHLHFDHAGNGAFINTPIIVQ 124
DB 92 APLFAYQKVVPAARDQLDAAGIRVDR-----ILLSHAHWDHAGS---LVDFPEVPV 138
QY 125 RAEEYAAQHSSEYILKECILPN-----LNYKI-----IEGDYEVVPGVQL 163
DB 139 WAPYEETAFSRIATPPAFAFPSPQFRHGVWRVPYSPRPFMGDFDESLLDFGDRLV---L 194
QY 164 LHTPGHTPGHQSLLIETEKSGPVLITDASYTKENFE---NEVPFAG-----FDSSELALSS 216
DB 195 VPLPGHTPGSVGLFVLDGSRUUFFGDTGTSWRLEGVGEGRQKFFAGRALVDRDPARTLAQ 254
QY 217 IKELKEVVMKEKP--IVFFGHIDIEQERGCKVKVFPEYI 250
DB 255 LAKIR-LLLRSDRLSVIPAHADARVAALGYFFPHWL 289

RESULT 8
US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-835-268-62
Query Match 6.9%; Score 90.5; DB 1; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNILKRVGYEPEDLLYIISHLHFD----- 108
DB 366 QAQFNGKFKEQSSNSAWLPVLSNRVPEPRPGTCVNDTSNLPDVTLVNFIIRSHPLMDKAVN 425
QY 109 HAGNGAF-----INTPIIVORAEYEAQAHSSEYLKCEILPNLN--YKIIIE---GD--- 154
DB 426 HEHNPVYKRDVFTKLVDKIRIDL--NQEIYIVYVGNLGRYKIVQYRNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLITIDASYTKNFEN-----E 202
DB 484 KLLDIFEVAPNEAIQVMEI---SQRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537
QY 203 VPFAGFDSSEALS---SIKRLKEV-----VMKEKPIVFFGHDIQERGCKV--FP 247
DB 538 DPYCGWDKEANTCRPYELDLIQDVANETSDICDSSVLKKIIVVYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598
RESULT 10
US-09-060-692-62
; Sequence 62, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:

US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415)343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-62
Query Match 6.9%; Score 90.5; DB 1; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
QY 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNILKRVGYEPEDLLYIISHLHFD----- 108
DB 366 QAQFNGKFKEQSSNSAWLPVLSNRVPEPRPGTCVNDTSNLPDVTLVNFIIRSHPLMDKAVN 425
QY 109 HAGNGAF-----INTPIIVORAEYEAQAHSSEYLKCEILPNLN--YKIIIE---GD--- 154
DB 426 HEHNPVYKRDVFTKLVDKIRIDL--NQEIYIVYVGNLGRYKIVQYRNGESLS 483
QY 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLITIDASYTKNFEN-----E 202
DB 484 KLLDIFEVAPNEAIQVMEI---SQRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537
QY 203 VPFAGFDSSEALS---SIKRLKEV-----VMKEKPIVFFGHDIQERGCKV--FP 247
DB 538 DPYCGWDKEANTCRPYELDLIQDVANETSDICDSSVLKKIIVVYQGSV--HLGCFVKIP 595
QY 248 EYI 250
DB 596 EVL 598
RESULT 9
US-08-835-268-62
; Sequence 62, Application US/08835268
; Patent No. 5807826

APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,692
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-692-62

Query Match 6.9%; Score 90.5; DB 2; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
Qy 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFD--- 108
Db 366 QAAFNGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDVLNFIIRSHPLMDKAVN 425
Qy 109 HAGNGAF-----INTPIIVORAEYEAQHSEYKCEILPNLN--YKIE-----GD--- 154
Db 426 HEHNNPVYKRDVFTKLVDKIRIDIL--NQEYIVYVVGTLNGLRIYKIVQYRNGESLS 483
Qy 155 -----YEWVP--GVQLLHTPGTHGOSLLIETEKSGPVLITIDASYTKENFEN-----E 202
Db 484 KLLDIFVAPNEALQWMEI-----SOTRKSLYIGTDHR---IKQIDLAMCNRYYNCFRCVR 537
Qy 203 VPAGFDSSELALS---SIKRLKEY-----VMKEKPIVFFGHDIQEGERCKV-FP 247
Db 538 DPYCGWDKEATCRPYELDLLQDVANETSDICDSSVLKKKIVVYTGQSV--HLGCFVKIP 595
Qy 248 EYI 250
Db 596 EVL 598

RESULT 11

US-08-833-391-62
; Sequence 62, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/833,391
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-833-391-62

Query Match 6.9%; Score 90.5; DB 3; Length 724;
Best Local Similarity 22.2%; Pred. No. 0.83;
Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;
Qy 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFD--- 108
Db 366 QAAFNGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDVLNFIIRSHPLMDKAVN 425
Qy 109 HAGNGAF-----INTPIIVORAEYEAQHSEYKCEILPNLN--YKIE-----GD--- 154
Db 426 HEHNNPVYKRDVFTKLVDKIRIDIL--NQEYIVYVVGTLNGLRIYKIVQYRNGESLS 483
Qy 155 -----YEWVP--GVQLLHTPGTHGOSLLIETEKSGPVLITIDASYTKENFEN-----E 202
Db 484 KLLDIFVAPNEALQWMEI-----SOTRKSLYIGTDHR---IKQIDLAMCNRYYNCFRCVR 537
Qy 203 VPAGFDSSELALS---SIKRLKEY-----VMKEKPIVFFGHDIQEGERCKV-FP 247
Db 538 DPYCGWDKEATCRPYELDLLQDVANETSDICDSSVLKKKIVVYTGQSV--HLGCFVKIP 595
Qy 248 EYI 250
Db 596 EVL 598

RESULT 12

US-09-060-610-62
; Sequence 62, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,268
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELEPHONE: (415) 343-4341
TELEFAX: (415) 343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10151A-62

Query Match 6.9%; Score 90.5; DB 4; Length 724;

Best Local Similarity 22.2%; Pred. No. 0.83;

Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;

Qy 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLRKVGYPEPDLIISSHLHFD---- 108

Db 366 QAAFGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDTVLNFIKSHPLMDKAVN 425

Qy 109 HAGNGAF-----INTPIIVORAEYAAQHSSEYKLCILPNLN--YKIIIE---GD--- 154

Db 426 HEHNNPVYKRDIVFTKLVDKIRIDIL--NQEIYIVYVGTNLGRIVKIQVYRNGESLS 483

Qy 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLTTIDASYTKENFEN-----E 202

Db 484 KLLDIEVAPNEAIQWMEI---SQTRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537

Qy 203 VPAGFDSLEALS---SIKELKEV-----VMKEKPIVFFGHDIQEERGCKV-PP 247

Db 538 DPYCGMDKEANTCRPYELDLQDVANETSDICDSSVLKKKIVVTYQGSV--HLGCFVKIP 595

Qy 248 EYI 250

Db 596 EVL 598

RESULT 13

PCT-US94-10151A-62

Sequence 62, Application PC/TUS9410151A

GENERAL INFORMATION:

APPLICANT: The Regents of the University of California

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR HOBBACH TEST ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10151A-62

Query Match 6.9%; Score 90.5; DB 5; Length 724;

Best Local Similarity 22.2%; Pred. No. 0.83;

Matches 54; Conservative 39; Mismatches 87; Indels 63; Gaps 15;

Qy 61 EGLFNGTFVEGQ-----VLPKMTEDRIVNLRKVGYPEPDLIISSHLHFD---- 108

Db 366 QAAFGKFKQSSNSAWLPVLSRVPEPRPGTCVNDTSNLPDTVLNFIKSHPLMDKAVN 425

Qy 109 HAGNGAF-----INTPIIVORAEYAAQHSSEYKLCILPNLN--YKIIIE---GD--- 154

Db 426 HEHNNPVYKRDIVFTKLVDKIRIDIL--NQEIYIVYVGTNLGRIVKIQVYRNGESLS 483

Qy 155 -----YEVVP--GVQLLHTPGHTPGHOSLLIETKSGPVLTTIDASYTKENFEN-----E 202

Db 484 KLLDIEVAPNEAIQWMEI---SQTRKSLYIGTDHR---IKQIDLAMCNRYYDNCRCVR 537

Qy 203 VPAGFDSLEALS---SIKELKEV-----VMKEKPIVFFGHDIQEERGCKV-PP 247

Db 538 DPYCGMDKEANTCRPYELDLQDVANETSDICDSSVLKKKIVVTYQGSV--HLGCFVKIP 595

Qy 248 EYI 250

Db 596 EVL 598

RESULT 14

US-08-738-944-50

Sequence 50, Application US/08738944

Patent No. 5783431

GENERAL INFORMATION:

APPLICANT: Peterson, et al.

TITLE OF INVENTION: METHODS FOR GENERATING AND

TITLE OF INVENTION: SCREENING NOVEL METABOLIC PATHWAYS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas

CITY: New York

STATE: NY

COUNTRY: USA

ZIP: 10036/2711

COMPUTER READABLE FORM:

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 20, 2004, 16:18:56 ; Search time 41 Seconds
(without alignments)
967.845 Million cell updates/sec

Title: US-10-019-661-2

Perfect score: 1315

Sequence: 1 MTVKLLFVPAGRCMLDHS.....VFFGHDIQERCKVFPEYI 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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20: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA1999.DAT.*
21: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2000.DAT.*
22: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*
24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1315	100.0	250	22 AAB50476	Listeria sp. stral
2	1304	99.2	248	23 AAU78814	Bacillus sp. Autol
3	1244	94.6	250	23 AAU78808	Autoinducer inacti
4	1228	93.4	250	23 AAU78807	Autoinducer inacti
5	1219	92.7	250	23 AAU78804	Autoinducer inacti
6	1213	92.2	250	23 AAU78806	Autoinducer inacti
7	1212	92.2	250	23 AAU78809	Autoinducer inacti
8	1212	92.2	250	23 AAU78811	Autoinducer inacti
9	1209	91.9	250	23 AAU78810	Autoinducer inacti

10	1202	91.4	250	23 AAU78805	Autoinducer inacti
11	1200	91.3	250	23 AAU78812	Autoinducer inacti
12	311	23.7	263	23 AAU78815	Autoinducer inacti
13	145.5	11.1	283	23 ABA48771	Listeria monocytog
14	141	10.7	222	22 AAB96283	Putative P. abyss
15	135.5	10.3	281	22 AAB73541	Burkholderia cepac
16	135.5	10.3	285	21 AAG30597	Arabidopsis thalia
17	135.5	10.3	324	21 AAG30596	Arabidopsis thalia
18	133	10.1	204	22 AAB96055	Putative P. abyss
19	123.5	9.4	285	23 ABB90340	Human polypeptide
20	119.5	9.1	238	23 ABB49158	Listeria monocytog
21	119	9.0	288	22 AAB67569	Amino acid sequenc
22	119	9.0	298	20 AAY73880	Human prostate tum
23	119	9.0	298	21 AAB43779	Human cancer assoc
24	119	9.0	298	22 AAU23487	Novel human enzyme
25	119	9.0	298	22 AAM25792	Human protein sequ
26	118.5	9.0	323	23 ABP51438	Human MDP1 SEQ ID
27	117.5	8.9	331	21 AAG10298	Arabidopsis thalia
28	117	8.9	288	21 AAG10299	Arabidopsis thalia
29	115	8.7	220	21 AAG10300	Arabidopsis thalia
30	114.5	8.7	281	21 AAG41447	Arabidopsis thalia
31	114.5	8.7	286	21 AAG41446	Arabidopsis thalia
32	114.5	8.7	331	21 AAG41445	Arabidopsis thalia
33	113.5	8.6	252	21 AAG31661	Arabidopsis thalia
34	112	8.5	210	23 ABB53851	Arabidopsis thalia
35	109	8.3	361	21 AAY71110	Lactococcus lactis
36	109	8.3	361	23 AAU83595	Human Hydrolase pr
37	109	8.3	385	22 AAM78721	Human PRO protein,
38	108	8.2	228	22 ABB64252	Human protein SEQ
39	106	8.1	209	23 ABP38792	Drosophila melanog
40	105	8.0	271	22 ABB67381	Staphylococcus epi
41	105	8.0	305	22 ABB71300	Drosophila melanog
42	102.5	7.8	282	23 ABU65074	Drosophila melanog
43	101.5	7.7	258	21 AAG10987	Human NOV17d prote
44	101.5	7.7	268	21 AAG10986	Arabidopsis thalia
45	101.5	7.7	282	23 ABU65072	Arabidopsis thalia
					Human NOV17b prote

ALIGNMENTS

RESULT 1

AAB50476
ID AAB50476 standard; Protein; 250 AA.
XX AAB50476;

XX AC

XX DT

XX DT 10-APR-2001 (first entry)

XX DE Listeria sp. strain 240B1 AiiA.

XX DE

XX XX

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XX XX

PT reducing bacterial damage to a plant or animal, or treating bacterial
PT infections in animals -
PS Claim 6; Fig 4B; 49pp; English.
XX The present sequence is a bacterial autoinducer inactivation protein
CC (AiiA). It is useful for increasing disease resistance as well as
CC preventing or reducing bacterial damage to a plant or animal. The nucleic
CC acid encoding the AiiA protein may be used to confer resistance to
CC diseases where expression of pathogenic genes are regulated by
CC autoinducers, such as diseases caused by *Pseudomonas aeruginosa*, *Erwinia*
CC *stewartii*, *Xenorhabdus nematophilus*, *Erwinia chrysanthemi*, *Pseudomonas*
CC *solanacearum* and *Xanthomonas campestris*. It may also be used to confer
CC soft rot disease resistance in susceptible plants such as potato,
CC eggplant, Chinese cabbage, carrot and celery. The bacterial autoinducer
CC inactivation protein may be directly used to treat or prevent bacterial
CC infections in animals including humans.

SQ Sequence 250 AA;

Query Match 100.0%; Score 1315; DB 22; Length 250;
Best Local Similarity 100.0%; Pred. No. 1.6e-134;
Matches 250; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWKLYFVAGRCMLDSSVNSTLTPEGLDLPVWCYLLETEGPIIVDTGMPESAVNN 60
DB 1 MTWKLYFVAGRCMLDSSVNSTLTPEGLDLPVWCYLLETEGPIIVDTGMPESAVNN 60
QY 61 EGLFNGTFFVGGVLPKMTEDRIVNLRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFFVGGVLPKMTEDRIVNLRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVORAEYEAQHSEYLYKECILPNLNKYIEGDIYVVPVGVQLLHTPGHTPGHOSLLIET 180
DB 121 IIIVORAEYEAQHSEYLYKECILPNLNKYIEGDIYVVPVGVQLLHTPGHTPGHOSLLIET 180
QY 181 EKSGPVLLTTDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLLTTDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
QY 241 RGCKVFPEYI 250
DB 241 RGCKVFPEYI 250

RESULT 2
AAU78814
ID AAU78814 standard; Protein; 248 AA.
XX
AC AAU78814;
XX
DT 18-JUN-2002 (first entry)
XX
DE Bacillus sp. Autoinducer inactivation protein, AiiA.

XX Autoinducer inactivation; AiiA; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.
XX
OS Bacillus sp. 240B1.
XX
FN WO200216623-Al.
XX
PD 28-FEB-2002.
XX
PF 23-AUG-2000; 2000WO-SG00123.
XX
PR 23-AUG-2000; 2000WO-SG00123.
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
XX Zhang L, Dong Y, Xu J;

DR WPI; 2002-304123/34.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to
PT a disease in sustainable plant or animal and for reducing bacterial
PT damage -
XX
PS Example 2; Fig 6; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an

CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the *Bacillus* sp. 240B1 autoinducer
CC inactivation protein AiiA, a putative metallohydrolase and autoinducer
CC inactivation protein.

XX Sequence 248 AA;

Query Match 99.2%; Score 1304; DB 23; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.5e-133;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTWKLYFVAGRCMLDSSVNSTLTPEGLDLPVWCYLLETEGPIIVDTGMPESAVNN 60
DB 1 MTWKLYFVAGRCMLDSSVNSTLTPEGLDLPVWCYLLETEGPIIVDTGMPESAVNN 60
QY 61 EGLFNGTFFVGGVLPKMTEDRIVNLRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFFVGGVLPKMTEDRIVNLRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
QY 121 IIIVORAEYEAQHSEYLYKECILPNLNKYIEGDIYVVPVGVQLLHTPGHTPGHOSLLIET 180
DB 121 IIIVORAEYEAQHSEYLYKECILPNLNKYIEGDIYVVPVGVQLLHTPGHTPGHOSLLIET 180
QY 181 EKSGPVLLTTDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
DB 181 EKSGPVLLTTDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
QY 241 RGCKVFPE 248
DB 241 RGCKVFPE 248

RESULT 3
AAU78808
ID AAU78808 standard; Protein; 250 AA.
XX
AC AAU78808;
XX
DT 18-JUN-2002 (first entry)
XX
DE Autoinducer inactivation protein AiiG.

XX Autoinducer inactivation; AiiG; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.
XX
OS Bacillus thuringiensis B18.
XX
FN WO200216623-Al.
XX
PD 28-FEB-2002.
XX

PF 23-AUG-2000; 2000WO-SG00123.
 XX
 PR 23-AUG-2000; 2000WO-SG00123.
 XX
 PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
 XX
 PI Zhang L, Dong Y, Xu J;
 XX
 DR WPI; 2002-304123/34.
 DR N-PSDB; ABK4742.
 XX
 XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX
 PS Claim 17; Fig 9; 82pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein.
 CC AiiG, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX
 SQ Sequence 250 AA;
 Query Match 94.6%; Score 1244; DB 23; Length 250;
 Best Local Similarity 92.8%; Pred. No. 8.7e-127;
 Matches 232; Conservative 13; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MTVKKLYFVPAGRCMLDHSVNSTLTGELLDLFVWCYLLTEEGPILVDTGMPESAVNN 60
 DB 1 MTVKKLYFVPAGRCMLDHSVNSALTGKLLNLPVWCYLLTEEGPILVDTGMPESAVNN 60
 QY 61 EGLFNGTFVEGQVLPMKTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 DB 61 EGLFNGTFVAKGQILPKMTEEDRIVTILKRAYEPDLDLYIISSHLHFDHAGNGAFINTP 120
 QY 121 IIVQRAEYEAQHSEEVYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHQSLLIET 180
 DB 121 IIVQRAEYEAQHSEEVYLKECILPDLNLYKIIEGDYEVVPGVRLLYTPGHSPGHQSLLIET 180
 QY 181 EKSGPVLTTIDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
 DB 181 EKSGPVLTTIDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
 QY 241 RGCKVFPPEYI 250
 DB 241 KGCKVFPPEYI 250
 RESULT 4
 AAU78807
 ID AAU78807 standard; Protein; 250 AA.
 XX
 AC AAU78807;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Autoinducer inactivation protein AiiF.
 XX
 KW Autoinducer inactivation; AiiF; N-acyl-homoserine lactone;

KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; *Erwinia carotovora*.
 XX
 OS *Bacillus thuringiensis* B17.
 XX
 PN WO200216623-A1.
 XX
 PD 28-FEB-2002.
 XX
 PF 23-AUG-2000; 2000WO-SG00123.
 XX
 PR 23-AUG-2000; 2000WO-SG00123.
 XX
 PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
 XX
 PI Zhang L, Dong Y, Xu J;
 XX
 DR WPI; 2002-304123/34.
 DR N-PSDB; ABK47471.
 XX
 PT Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX
 PS Claim 17; Fig 9; 82pp; English.
 XX
 CC The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein.
 CC AiiF, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX
 SQ Sequence 250 AA;
 Query Match 93.4%; Score 1228; DB 23; Length 250;
 Best Local Similarity 92.8%; Pred. No. 4.8e-125;
 Matches 232; Conservative 10; Mismatches 8; Indels 0; Gaps 0;
 QY 1 MTVKKLYFVPAGRCMLDHSVNSTLTGELLDLFVWCYLLTEEGPILVDTGMPESAVNN 60
 DB 1 MTVKKLYFVPAGRCMLDHSVNSTLTAPGNLLNLPVWCYLLTEEGPILVDTGMPESAVNN 60
 QY 61 EGLFNGTFVEGQVLPMKTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 DB 61 EGLFNGTFVEGQILPKMTEEDRIVNILKRVGYEPDLDLYIISSHLHFDHAGNGAFINTP 120
 QY 121 IIVQRAEYEAQHSEEVYLKECILPNLNYKIIEGDYEVVPGVQLLHTPGHQSLLIET 180
 DB 121 IIVQREYEAALHREYMKECILPHNLNYKIIEGDYEVVPGVQLLYTPGHSPGHQSLLIET 180
 QY 181 EKSGPVLTTIDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
 DB 181 EKSGPVLTTIDASYTKENFENFVFPAGFDSSELALSSIKRLKEVVMKEKPIVFFGHDIQE 240
 QY 241 RGCKVFPPEYI 250
 DB 241 KGKVPPEYI 250
 RESULT 5
 AAU78804

ID	AAU78804 standard; Protein; 250 AA.	
XX		
AC	AAU78804;	
XX		
DT	18-JUN-2002 (first entry)	
XX		
XX	Autoinducer inactivation protein AiiC.	
XX		
KW	Autoinducer inactivation; AiiC; N-acyl-homoserine lactone;	
KW	disease resistance; bacterial damage reduction; biofilm;	
KW	potato soft rot disease; Erwinia carotovora.	
XX		
OS	Bacillus thuringiensis Cot1.	
XX		
PN	W0200216623-A1.	
XX		
PD	28-FEB-2002.	
XX		
PF	23-AUG-2000; 2000WO-SG00123.	
XX		
PR	23-AUG-2000; 2000WO-SG00123.	
XX		
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.	
XX		
PI	Zhang L, Dong Y, Xu J;	
XX		
DR	WPI; 2002-304123/34.	
DR	N-PSDB; ABK47468.	
XX		
PT	Polynucleotide encoding autoinducer inactivation protein, bacterium	
PT	having polynucleotide, and protein useful for increasing resistance to	
PT	a disease in sustainable plant or animal and for reducing bacterial	
PT	damage -	
XX		
PS	Claim 17; Fig 8; 82pp; English.	
XX		
CC	The invention describes an isolated polynucleotide encoding an	
CC	autoinducer (N-acyl-homoserine lactone) inactivation protein. The	
CC	polynucleotide is useful for increasing disease resistance in a plant or	
CC	animal by introducing a polynucleotide into a cell of such a plant or	
CC	animal, in a manner that allows the cell to express the gene. The protein	
CC	is useful for reducing bacterial damage to a plant or animal preferably	
CC	human; and for reducing the formation of bacterial biofilms, by exposing	
CC	biofilm-forming bacteria to the autoinducer inactivation protein. A	
CC	bacterial cell transformed with the polynucleotide, especially a plant or	
CC	animal bacterium preferably Bacillus thuringiensis which is from B1, B2,	
CC	B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a	
CC	disease in a susceptible plant or animal, where virulence is regulated by	
CC	autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.	
CC	This is the amino acid sequence of the autoinducer inactivation protein	
CC	AiiC, the autoinducer inactivation activity of which is studied in the	
XX		
XX	Sequence 250 AA;	
XX		
XX	Query Match 92.7%; Score 1219; DB 23; Length 250;	
XX	Best Local Similarity 91.2%; Pred. No. 4.6e-124;	
XX	Matches 228; Conservative 12; Mismatches 10; Indels 0; Gaps 0;	
QY	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
DB	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60	
QY	61 EGLFNGTFVGGVLPKMTTEEDRVNILKRVGYEPEDLLYIISSHLHFHAGNGAFINTP 120	
DB	61 ENLFEGTFAEGQILPQMTTEEDRIAILKRAGYEPDLLYIISSHLHFHAGNGAFINTP 120	
QY	121 IIVQAEYEAQAQSHSEYKCECILPNLYKIIEGDYVVPVQVLLHTPGHPTGHQSLLIET 180	
DB	121 IIVQAEYEAQAQREYKCECILPNLYKIIEGDYVVPVQVLLHTPGHPTGHQSLLIET 180	
QY	181 EKSGVLLTIDASYTKENFENEPVPAAGFDPSELALSSIKRLKEYVMKEKPLVFFGHDIQE 240	

Db	181 EKSGVLLTIDASYTKENFENEPVPAAGFDPSELALSSIKRLKEYVMKEKPLVFFGHDIQE 240	
QY	241 RGCKVPEYI 250	
DB	241 KGCKVPEYI 250	

RESULT 6

AAU78806	
ID	AAU78806 standard; Protein; 250 AA.
XX	
AC	AAU78806;
XX	
DT	18-JUN-2002 (first entry)
XX	
XX	Autoinducer inactivation protein AiiE.
DE	
XX	
KW	Autoinducer inactivation; AiiE; N-acyl-homoserine lactone;
KW	disease resistance; bacterial damage reduction; biofilm;
KW	potato soft rot disease; Erwinia carotovora.
XX	
OS	Bacillus thuringiensis B2.
XX	
PN	W0200216623-A1.
XX	
PD	28-FEB-2002.
XX	
PF	23-AUG-2000; 2000WO-SG00123.
XX	
PR	23-AUG-2000; 2000WO-SG00123.
XX	
PA	(MOLE-) INST MOLECULAR AGROBIOLOGY.
XX	
PI	Zhang L, Dong Y, Xu J;
XX	
DR	WPI; 2002-304123/34.
DR	N-PSDB; ABK47470.
XX	
PT	Polynucleotide encoding autoinducer inactivation protein, bacterium
PT	having polynucleotide, and protein useful for increasing resistance to
PT	a disease in sustainable plant or animal and for reducing bacterial
PT	damage -
XX	
PS	Claim 17; Fig 9; 82pp; English.
XX	
CC	The invention describes an isolated polynucleotide encoding an
CC	autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC	polynucleotide is useful for increasing disease resistance in a plant or
CC	animal by introducing a polynucleotide into a cell of such a plant or
CC	animal, in a manner that allows the cell to express the gene. The protein
CC	is useful for reducing bacterial damage to a plant or animal preferably
CC	human; and for reducing the formation of bacterial biofilms, by exposing
CC	biofilm-forming bacteria to the autoinducer inactivation protein. A
CC	bacterial cell transformed with the polynucleotide, especially a plant or
CC	animal bacterium preferably Bacillus thuringiensis which is from B1, B2,
CC	B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC	disease in a susceptible plant or animal, where virulence is regulated by
CC	autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.
CC	This is the amino acid sequence of the autoinducer inactivation protein
CC	AiiE, the autoinducer inactivation activity of which is studied in the
XX	
XX	Sequence 250 AA;
XX	
XX	Query Match 92.2%; Score 1213; DB 23; Length 250;
XX	Best Local Similarity 90.4%; Pred. No. 2.1e-123;
XX	Matches 226; Conservative 14; Mismatches 10; Indels 0; Gaps 0;
QY	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
DB	1 MTVKKLYFVPAACRMLDHSVNSTLTPGELLDPVWCYLLETEEGPILVDTGMPESAVNN 60
QY	61 EGLFNGTFVGGVLPKMTTEEDRVNILKRVGYEPEDLLYIISSHLHFHAGNGAFINTP 120

Db 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 QY 121 IIVQRAEYEAQHSEYLYKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 Db 121 IIVQTEYEAALHREYMKECILPHLYKIIEGDYEVVPGVQLLHTPGHSPGHQSILFIET 180
 QY 181 EKSGLVLLTIDASYTKENFENEVPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EKSGLVLLTIDASYTKENFENEVPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250

RESULT 7

AAU78809
 ID AAU78809 standard; Protein; 250 AA.

AC AAU78809;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiH.

XX Autoinducer inactivation; AiiH; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; Erwinia carotovora.

OS Bacillus thuringiensis B20.

PN WO200216623-A1.

PD 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47473.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -

XX Claim 17; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably Bacillus thuringiensis, which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by Erwinia carotovora.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiH, the autoinducer inactivation activity of which is studied in the
 CC invention.

XX Sequence 250 AA;

Query Match 92.2%; Score 1212; DB 23; Length 250;
 Best Local Similarity 90.8%; Pred. No. 2.7e-123;
 Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MTVKKLYFVPGRCMLDHSVSNSTLTGCELLDLPVWCYLLTEEGPILVDTGMPESAVNN 60
 Db 1 MTVKKLYFVPGRCMLDHSVSNSTLTGCELLDLPVWCYLLTEEGPILVDTGMPESAVNN 60
 QY 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 Db 61 EGLFNGTVEGQILPMTTEEDRIIVNLKRVGYEPDPLLIISSHLHFDHAGNGAFTNTP 120
 QY 121 IIVQRAEYEAQHSEYLYKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLIET 180
 Db 121 IIVQRAEYEAALHREYMKECILPHLYKIIEGDYEVVPGVQLLHTPGHSPGHQSILFIET 180
 QY 181 EKSGLVLLTIDASYTKENFENEVPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EKSGLVLLTIDASYTKENFENEVPAGPDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250

RESULT 8

AAU78811

ID AAU78811 standard; Protein; 250 AA.

AC AAU78811;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiJ.

XX Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; Erwinia carotovora.

OS Bacillus thuringiensis B22.

PN WO200216623-A1.

PD 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47475.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT a disease in sustainable plant or animal and for reducing bacterial
 PT damage -

XX Claim 17; Fig 9; 82pp; English.

XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably Bacillus thuringiensis, which is from B1, B2,

CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the autoinducer inactivation protein
CC AiiJ, the autoinducer inactivation activity of which is studied in the
CC invention.

XX Sequence 250 AA;

Query Match 92.2%; Score 1212; DB 23; Length 250;
Best Local Similarity 90.8%; Pred. No. 2.7e-123;
Matches 227; Conservative 13; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTVKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEGPIIVDTGMPESAVNN 60
DB 1 MTVKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEGPIIVDTGMPESAVNN 60

QY 61 EGLFNGTFVGGVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFVGGVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

QY 121 IIVQAEYEAQHSEYKCEILPNLNYKIEGDEYVVPVGVQLLHTPGHTPGHQSLLIET 180
DB 121 IIVQAEYEAALHREYKCEILPHLNKIEGDEYVVPVGVQLLHTPGHSPGHQSLLFIET 180

QY 181 EKSGPVLLTTDASYTKENFENFVDFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
DB 181 EQSGVLLTTDASYTKENFENFVDFAGFDPPELALSSIKRLKGVVAEEKPIVFFGHDIQEQ 240

QY 241 RGCKVFPEYI 250
DB 241 KGCRVFPEYI 250

RESULT 9
AAU78810
ID AAU78810 standard; Protein; 250 AA.

XX AC AAU78810;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiJ.

XX Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.

XX *Bacillus thuringiensis* B21.

XX WO200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47474.

XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PT having polynucleotide, and protein useful for increasing resistance to
PT a disease in sustainable plant or animal and for reducing bacterial
PT damage -
XX
XX Claim 17; Fig 9; 82pp; English.
XX
XX The invention describes an isolated polynucleotide encoding an

CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
CC polynucleotide is useful for increasing disease resistance in a plant or
CC animal by introducing a polynucleotide into a cell of such a plant or
CC animal, in a manner that allows the cell to express the gene. The protein
CC is useful for reducing bacterial damage to a plant or animal, preferably
CC human; and for reducing the formation of bacterial biofilms, by exposing
CC biofilm-forming bacteria to the autoinducer inactivation protein. A
CC bacterial cell transformed with the polynucleotide, especially a plant or
CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
CC disease in a susceptible plant or animal, where virulence is regulated by
CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
CC This is the amino acid sequence of the autoinducer inactivation protein
CC AiiJ, the autoinducer inactivation activity of which is studied in the
CC invention.

XX Sequence 250 AA;

Query Match 91.9%; Score 1209; DB 23; Length 250;
Best Local Similarity 90.8%; Pred. No. 5.7e-123;
Matches 227; Conservative 12; Mismatches 11; Indels 0; Gaps 0;

QY 1 MTVKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEGPIIVDTGMPESAVNN 60
DB 1 MTVKLYFVAGRCMLDSSVNSTLTGCELLDLPVWCYLLTEGPIIVDTGMPESAVNN 60

QY 61 EGLFNGTFVGGVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
DB 61 EGLFNGTFVGGVLPKMTEDRIVNLIKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120

QY 121 IIVQAEYEAQHSEYKCEILPNLNYKIEGDEYVVPVGVQLLHTPGHTPGHQSLLIET 180
DB 121 IIVQAEYEAALHREYKCEILPHLNKIEGDEYVVPVGVQLLHTPGHSPGHQSLLFIET 180

QY 181 EKSGPVLLTTDASYTKENFENFVDFAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQEQ 240
DB 181 DNGSVLLTTDASYTKENFENFVDFAGFDPPELALSSIKRLKGVVAEEKPIVFFGHDIQEQ 240

QY 241 RGCKVFPEYI 250
DB 241 KGCRVFPEYI 250

RESULT 10
AAU78805
ID AAU78805 standard; Protein; 250 AA.

XX AC AAU78805;

DT 18-JUN-2002 (first entry)

DE Autoinducer inactivation protein AiiJ.

XX Autoinducer inactivation; AiiJ; N-acyl-homoserine lactone;
KW disease resistance; bacterial damage reduction; biofilm;
KW potato soft rot disease; *Erwinia carotovora*.

XX *Bacillus thuringiensis* B1.

XX WO200216623-A1.

XX 28-FEB-2002.

XX 23-AUG-2000; 2000WO-SG00123.

XX 23-AUG-2000; 2000WO-SG00123.

XX (MOLE-) INST MOLECULAR AGROBIOLOGY.

XX Zhang L, Dong Y, Xu J;

XX WPI; 2002-304123/34.

XX N-PSDB; ABK47469.

XX PT Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT damage in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX Claim 17; Fig 9; 82pp; English.
 XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiD, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX SQ Sequence 250 AA;
 Query Match 91.4%; Score 1202; DB 23; Length 250;
 Best Local Similarity 89.6%; Pred. No. 3.3e-122;
 Matches 224; Conservative 14; Mismatches 12; Indels 0; Gaps 0;
 QY 1 MTVKLYFVPAGRCLMDHSSVNSTLTGCELDLPVWCYLLETEGPIILVDTGMPESAVNN 60
 Db 1 MTVKLYFIPAGRCMLDHSVNSAUTPGKLNLPVWCYLLETEGPIILVDTGMPESAVNN 60
 QY 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 QY 121 IIVQRAEYEAQHSEYVKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLTET 180
 Db 121 IIVQRTYEYEAALHREYMKECILPHLYNKIIEGDYEVVPGVQLLHTPGHSPHQSLLFTET 180
 QY 181 EKSGPVLLTTIDASYTKENFENFVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EQSGSVLLTIDASYTKENFENFVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250
 RESULT 11
 AAU78812
 ID AAU78812 standard; Protein; 250 AA.
 XX AAU78812;
 AC AAU78812;
 DT 18-JUN-2002 (first entry)
 DE Autoinducer inactivation protein AiiK.
 KW Autoinducer inactivation; AiiK; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;
 KW potato soft rot disease; *Erwinia carotovora*.
 OS *Bacillus thuringiensis* B25.
 XX WO200216623-A1.
 PN 28-FEB-2002.
 PD 23-AUG-2000; 2000WO-SG00123.

XX PR 23-AUG-2000; 2000WO-SG00123.
 XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
 PA Zhang L, Dong Y, Xu J;
 PI WPI; 2002-304123/34.
 DR N-PSDB; ABK47476.
 XX Polynucleotide encoding autoinducer inactivation protein, bacterium
 PT having polynucleotide, and protein useful for increasing resistance to
 PT damage in sustainable plant or animal and for reducing bacterial
 PT damage -
 XX Claim 17; Fig 9; 82pp; English.
 XX The invention describes an isolated polynucleotide encoding an
 CC autoinducer (N-acyl-homoserine lactone) inactivation protein. The
 CC polynucleotide is useful for increasing disease resistance in a plant or
 CC animal by introducing a polynucleotide into a cell of such a plant or
 CC animal, in a manner that allows the cell to express the gene. The protein
 CC is useful for reducing bacterial damage to a plant or animal preferably
 CC human; and for reducing the formation of bacterial biofilms, by exposing
 CC biofilm-forming bacteria to the autoinducer inactivation protein. A
 CC bacterial cell transformed with the polynucleotide, especially a plant or
 CC animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2,
 CC B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a
 CC disease in a susceptible plant or animal, where virulence is regulated by
 CC autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*.
 CC This is the amino acid sequence of the autoinducer inactivation protein
 CC AiiK, the autoinducer inactivation activity of which is studied in the
 CC invention.
 XX SQ Sequence 250 AA;
 Query Match 91.3%; Score 1200; DB 23; Length 250;
 Best Local Similarity 90.0%; Pred. No. 5.4e-122;
 Matches 225; Conservative 12; Mismatches 13; Indels 0; Gaps 0;
 QY 1 MTVKLYFVPAGRCLMDHSSVNSTLTGCELDLPVWCYLLETEGPIILVDTGMPESAVNN 60
 Db 1 MTVKLYFIPAGRCMLDHSVNSGTAPGNLNLFPWCYLLETEGAILVDTGMPESAVNN 60
 QY 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 Db 61 EGLFNGTFVEGQVLPKMTTEEDRIVNILKRVGYEPEDLLYIISSHLHFDHAGNGAFINTP 120
 QY 121 IIVQRAEYEAQHSEYVKECILPNLYKIIEGDYEVVPGVQLLHTPGHTPGHQSLLTET 180
 Db 121 IIVQRTYEYEAALHREYMKECILPHLYNKIIEGDYEVVPGVQLLHTPGHSPHQSLLFTET 180
 QY 181 EKSGPVLLTTIDASYTKENFENFVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 Db 181 EQSGSVLLTIDASYTKENFENFVFPAGFDSALSSIKRLKEVVMKEKPIVFFGHDIQOE 240
 QY 241 RGCKVFPEYI 250
 Db 241 KSCRVFPEYI 250
 RESULT 12
 AAU78815
 ID AAU78815 standard; Protein; 263 AA.
 XX AAU78815;
 AC AAU78815;
 DT 18-JUN-2002 (first entry)
 DE Autoinducer inactivation protein AiiB.
 KW Autoinducer inactivation; AiiB; N-acyl-homoserine lactone;
 KW disease resistance; bacterial damage reduction; biofilm;

potato soft rot disease; *Erwinia carotovora*.
XX
XX Agrobacterium tumefaciens M103.
OS
XX WO200216623-A1.
PN
XX 28-FEB-2002.
PPD
XX 23-AUG-2000; 2000WO-SG00123.
PPF
XX 23-AUG-2000; 2000WO-SG00123.
PPN
XX (MOLE-) INST MOLECULAR AGROBIOLOGY.
PPA
XX Zhang L, Dong Y, Xu J;
PI PI WPI; 2002-304123/34.
PI PI N-PSDB; ABK47467.
XX
XX Polynucleotide encoding autoinducer inactivation protein, bacterium
PPT PPT having polynucleotide, and protein useful for increasing resistance to
PPT PPT a disease in sustainable plant or animal and for reducing bacterial
PT PT damage -
XX XX
Claim 17; Fig 4; 82pp; English.

The invention describes an isolated polynucleotide encoding an autoinducer (N-acyl-homoserine lactone) inactivation protein. The polynucleotide is useful for increasing disease resistance in a plant or animal by introducing a polynucleotide into a cell of such a plant or animal, in a manner that allows the cell to express the gene. The protein is useful for reducing bacterial damage to a plant or animal preferably human; and for reducing the formation of bacterial biofilms, by exposing biofilm-forming bacteria to the autoinducer inactivation protein. A bacterial cell transformed with the polynucleotide, especially a plant or animal bacterium preferably *Bacillus thuringiensis* which is from B1, B2, B17, B18, B20, B21, B22 and B25, is useful for increasing resistance to a disease in a susceptible plant or animal, where virulence is regulated by autoinducers e.g. potato soft rot disease caused by *Erwinia carotovora*. This is the amino acid sequence of the autoinducer inactivation protein AiiB, the autoinducer inactivation activity of which is studied in the invention.

Sequence 263 AA;

Query Match 23.7%; Score 311; DB 23; Length 263;
Best Local Similarity 32.1%; Pred.No. 4.3e-25;
Matches 84; Conservative 50; Mismatches 106; Indels 22; Gaps 9;

QY 5 KLYEVFAG--RCMLDHSSVNSTLTPGSELLDPVMCYLLETETEGFPILVDTCMP_ESAVNNE 61
Db :|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
5 RLYMLQSGTLTKCKVHNKKMQ--GNADYEIPVPFFLI THPGGHVTIDGGNAIEVATDPR 62
QY 62 GLFNGTFVEGOVLPKMTTEEDRIYNILKRGVYEPEDLLYIISSHLPFHAGNGAFINTPI 121
Db |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
63 GHWGG--ICDVYWFVLDKGQCVDIKALGFDPADVYVVQSHLUHL DHTGAIGRFPNATH 120
QY 122 IVORAEEAAQHSEYL-----KECILPLNLNYKII EG---DYEWVFG---VOLLHTPGH 169
Db |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
121 IVORSEYEAFTPDWFAGGGYIRKDFDKPGLKWQFLNGTQDDYVDYVGDTLTITFTPGH 180
QY 170 TPGHQSLILITEKSGPVLLTIDASYTKENFENFVFPAFDSEL--ALLSKRLKEVMKE 227
Db |||||||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
181 APGHSQILLVRLENPKLIIITDAAYTTLDHW E-EKALPGFLASTVDTVRSVKLRITYAEKH 239
QY 228 KPTVFFGHDLQEQRGCKVFPEY 249
Db |||||:|||:|||:|||:
240 DATVVTGHDPPAWANFKAPEF 261
XX XX

RESULT 13
ABBA48771 standard. Protein: 283 AA
TD 283

DB 160 WQENWLRIEGQIHTFTEKEFNDAIKMTHTCGHSHGVWLESD 204

RESULT 14
AAB96283
ID AAB96283 standard; Protein; 222 AA.

AC	AAB96283;
XX	
XX	
DT	29-OCT-2001 (first entry)
XX	
XX	
DE	Putative P. abyssi Zn-dependent hydrolase #4.
XX	
XX	
KW	Hyperthermophilic archaeon; hyperthermophilic protein.

OS *Pyrococcus abyssi*.

PN FR2792651-A1.

PD 27-OCT-2000.

21-APR-1999: 99ER-0005034

21-APR-1999: 99ER-0005034

XX (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.

PI Forterre P, Thierry JC, Prieur D, Dietrich J, LeCompte O;
PI Querellou J, Weissenbach J, Saurin W, Heilig R;
XX
DR WPI; 2001-126236/14.

PT New nucleotide sequences isolated from *Pyrococcus abyssi* encode
PT proteins useful in industry -
PT

PS Claim 7; Pages 941-942; 1657pp; French.

The present invention relates to the genomic sequence of *Pyrococcus abyssi* (see AF86431 and AAH41223-7) and *P. abyssi* proteins. *P. abyssi* is a hyperthermophilic archaeon, which is isolated from deep-sea hydrothermal vents. The present sequence is one such *P. abyssi* protein. The proteins of the present invention have various potential industrial uses, since the proteins are stable at very high temperatures, some up to 110 degrees centigrade.

CC Note: This patent is in the same patent family as WO2000065062, which
CC contains additional sequences as shown in AAB99132-AAB99143,
CC AAH75903-AAH75920 and AAG66436.

Sequence 222 AA:

Query Match	10.7%;	Score 141;	DB 22;	Length 222;
Best Local Similarity	25.3%;	Pred. No. 1.1e-06;		
Matches	55: Conservative	39: Mismatches	73: Indels	5

QY 22 NSTLTGELLDLPWCYLLETEEGPILVDTGMPESAVNNEGLNGTFVEGVLPKMTED 81
 | : | | | : : : : | | | : : |
db 9 NIIMLEGVNIDSNV--YPIKSKDEIPLVDTC-----TGYNNNVV LDTADSG 53

QY 82 RIVNLRKRVGVEPDLIISSHLHFDHAGNGAFINTPIIVQRAYE---EAAQHSEY 137

54	WLENVSK-----VILFNTHEHF	DHVGGLVFK	ELKVVEF	ASHKLTAKALEEGDDY	101
QY	138 LKECILP-----N	NYKII	EGDYEVVPG	---VOLHTPGH	CHOSTIETEKSG
					184

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105 I --- ILSYVYGRYPDPHEVELKLEDDG-ETKVGKVKTLRTH
Db

```

QY 185 PVLITDASYTKENFENEVPFAGDSEIALSSIKRIK 221

RESULT 15
AAB73541
ID AAB7.

AC AAB73541;

DT 07-AUG-2001 (first entry)

DE Burkholderia cepacia lipase production-enhancing protein. OrfC

AA Lipase production-enhancing protein; strain SC-20; OrfC;
KW open reading frame; expression cassette; vector; transformant;
KW drug intermediate production; agricultural chemical production.

OS Burkholderia cepacia.

JP2001008683-A.

16-JAN-2001.

XX 24-TTN-1999- 99,TP-0178948

XX 24-TTN-1999. 99.TD-0179948

XX
PA (SIMO) SIMTOMO CUEM CO LTDXX
WDT. 2001 075000/00

DR N-PSDB; AAH20222, AAH20223.

PT Lipase-production enhancing gene, used to produce lipase, for use in
PT the preparation of optically active compounds as intermediates for
PT drugs -

XX
PS
Claim 1: Fig 4-6: 31pp: Japanese

The invention relates to proteins (AAB73538-AAB73541) from Burkholderia cepacia which enhance the production of lipase, and the genes (AAH20219-AAH20222) encoding the lipase production-enhancing proteins. The genes of the invention were isolated from a 6.0 kb fragment of Burkholderia cepacia genomic DNA (AAH20223) which also contains the lipA gene which encodes a lipase (AAB73542). The invention also relates to expression cassettes, vectors, and transformants containing a gene of the invention and a lipase. The novel proteins and genes may be used in the production of lipase, which is for the preparation of optically active compounds such as intermediates for drugs and agricultural chemicals. The present sequence represents a Burkholderia cepacia SC-20 lipase production-enhancing protein, designated OrfC.

Sequence 281 AA:

Query Match	10.3%	Score 135.5;	DB 22;	Length 281;
Best Local Similarity	25.2%;	pred. No. 6.3e-06;		
Matches	54;	Conservative	28;	Mismatches 87;
				Indels 45;

QY 37 CYLLETEEGPILVDTCMPESAVNNEGLFNGTFVE--GQVLPMKMTEDRIVNILKRGVPEP 94
|||:: : | : || : | : | : | : | :
D6 58 CYYRGAGRTVLIIDAGA-----GGFRWGCGO-----LGNNALACGED 95

QY 95 EDLLVLISSHLHFDHAGG--NG-----AFINTPIIVQRABYEAAQHSEEVYLKECILPNLNY 148
 : : : | | | | | : | | : | | : | | : | | :

Db 96 AAIIDTILLTHAHPDHVVGLVNCAGETAPDNAELVWHPDPVCWEWDNDCT SPASGEADNCE 150

QY 149 KI-----IEGDYVVPGVQLLHTPGHTPGHQSLLIETEKSGPVLITDASYT 195

156 AVARRVFDAYGDRERLFEBBGQVLPGLDALPIPGHTDGH
196 KENEEN-EVDEA-CEDSEIATSSIKBIYENVMKVE 227

216 H1010RPEVSI AFDHDA SIAAATRSPIJDOVSSE 249

Search completed: February 20, 2004, 16:24:43
Job time : 43 secs
